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U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE ATTORNEY'S DOCKET NUMBER

**TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. §371**

SCH 1781

U.S. APPLICATION NO. (If known, see 37 CFR §1.5)

09/673840

INTERNATIONAL APPLICATION NO.

INTERNATIONAL FILING DATE

PCT/DE99/01163

15 April 1999

PRIORITY DATE CLAIMED

21 April 1998

TITLE OF INVENTION

HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BLADDER TISSUE

APPLICANT(S) FOR DO/EO/US

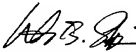
SPECHT, Thomas, et al.

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. §371.
 2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. §371.
 3. ☐ This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1).
 4. ☐ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
 5. ☒ A copy of the International Application as filed (35 U.S.C. §371(c)(2))
 - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☒ has been transmitted by the International Bureau.
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US)
 6. ☐ A translation of the International Application into English (35 U.S.C. §371(c)(2)).
 7. ☐ A copy of the International Search Report (PCT/ISA/210).
 8. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
 9. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)).
 10. ☐ An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)).
 11. ☐ A copy of the International Preliminary Examination Report (PCT/IPEA/409).
 12. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5)).
- Items 13. to 19. below concern document(s) or information included:**
13. ☐ An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98.
 14. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included
 15. ☐ A FIRST preliminary amendment.
 - ☐ A SECOND or SUBSEQUENT preliminary amendment.
 16. ☐ A substitute specification.
 17. ☐ A change of power of attorney and/or address letter.
 18. ☐ Certificate of Mailing by Express Mail
 19. ☒ Other items or information:

Sequence Listing with disk

COPY

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|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------|--------------|------------|---|-------------------------------|
| U.S. APPLICATION NO. 09/673840 INTERNATIONAL APPLICATION NO. PCT/DE99/01163 | ATTORNEY'S DOCKET NUMBER SCH 1781 | | | | |
| 17. <input checked="" type="checkbox"/> The following fees are submitted: BASIC NATIONAL FEE (37 CFR §1.492 (a) (1) - (5)): Search Report has been prepared by the EPO or JPO..... \$860.00 International preliminary examination fee paid to USPTO (37 CFR §1.482)..... \$690.00 No international preliminary examination fee paid to USPTO (37 CFR §1.482) but international search fee paid to USPTO (37 CFR §1.445(a)(2))..... \$710.00 Neither international preliminary examination fee (37 CFR §1.482) nor international search fee (37 CFR §1.445(a)(2)) paid to USPTO..... \$1,000.00 International preliminary examination fee paid to USPTO (37 CFR §1.482) and all claims satisfied provisions of PCT Article 33(2)-(4)..... \$100.00 | | | | | |
| ENTER APPROPRIATE BASIC FEE AMOUNT = \$860.00 | | | | | |
| Surcharge of \$130.00 for furnishing the oath or declaration later than months from the earliest claimed priority date (37 C.F.R. §1.492(e)). <input type="checkbox"/> 20 <input type="checkbox"/> 30 \$0.00 | | | | | |
| CLAIMS | NUMBER FILED | NUMBER EXTRA | RATE | | |
| Total claims | - 20 = | 0 | x \$ 18.00 | | \$0.00 |
| Independent claims | - 3 = | 0 | x \$ 80.00 | | \$0.00 |
| MULTIPLE DEPENDENT CLAIM(S) (if applicable) | | | | + | \$ 270.00 |
| TOTAL OF ABOVE CALCULATIONS = | | | | | \$860.00 |
| Reduction of 1/2 for filing by small entity, if applicable. A Verified Small Entity Statement must be filed (Note 37 C.F.R. §§1.9, 1.27, 1.28). | | | | | |
| SUBTOTAL = | | | | | \$0.00 |
| Processing fee of \$130.00 for furnishing the English translation later than months from the earliest claimed priority date (37 C.F.R. §1.492(f)). <input type="checkbox"/> 20 <input type="checkbox"/> 30 | | | | | |
| TOTAL NATIONAL FEE = | | | | | \$860.00 |
| Fee for recording the enclosed assignment (37 C.F.R. §1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. §§3.28, 3.31). \$40.00 per property. | | | | | |
| TOTAL FEES ENCLOSED = | | | | | \$860.00 |
| | | | | | Amount to be refunded: |
| | | | | | charged: |
| a <input checked="" type="checkbox"/> A check in the amount of \$860.00 to cover the above fees is enclosed. b <input type="checkbox"/> Please charge my Deposit Account No. <u>13-3402</u> in the amount of \$_____ to cover the above fees. A duplicate copy of this sheet is enclosed. c <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>13-3402</u> . A duplicate copy of this sheet is enclosed. | | | | | |
| NOTE: Where an appropriate time limit under 37 C.F.R. §§1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. §1.137(a) or (b)) must be filed and granted to restore the application to pending status. | | | | | |
| SEND ALL CORRESPONDENCE TO MILLEN, WHITE, ZELANO & BRANIGAN, P.C. Arlington Courthouse Plaza I 2200 Clarendon Boulevard, Suite 1400 Arlington, Virginia 22201 (703) 243-6333 | | | | | |
| Filed: October 23, 2000 | | | | | |
| AJZ(HBS): jmm k:\pat\sch\1781\natl phase transmtl | | | | | |
| SIGNATURE  Harry B. Shubin NAME | | | | | 32,004 REGISTRATION NUMBER |

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IN THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US)

International Application No. : PCT/DE99/01163
International Filing Date : 15 APRIL 1999
U.S. Serial No. : 09/673,840
Deposit Date U.S. Nat'l Phase : 23 OCTOBER 2000
Priority Date(s) Claimed : 21 APRIL 1998
Applicant(s) : SPECHT, Thomas, et al.
Title: HUMAN NUCLEIC ACID SEQUENCES OF NORMAL BLADDER TISSUE

PRELIMINARY AMENDMENT

Commissioner for Patents
Box PCT
Washington, D.C. 20231

Sir:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend as follows:

IN THE CLAIMS:

3. (Amended) Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2, characterized in that they are expressed elevated in normal bladder tissue.
4. (Amended) BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for use as vehicles for gene transfer.
5. (Amended) A nucleic acid sequence according to claim 1, wherein it has 90% homology to a human nucleic acid sequence.
6. (Amended) A nucleic acid sequence according to claim 1, wherein it has 95% homology to a human nucleic acid sequence.
7. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claim 1, in such a sufficient amount that they hybridize with the sequences according to claim 1.

8. (Amended) A nucleic acid sequence according to claim 1, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. (Amended) A nucleic acid sequence according to claim 1, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. (Amended) A nucleic acid sequence according to claim 1, which codes at least one partial sequence of a bioactive polypeptide.

11. (Amended) An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 1, together with at least one control or regulatory sequence.

13. (Amended) An expression cassette according to claim 11, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. (Amended) Use of nucleic acid sequences according to claim 1 for producing full-length genes.

16. (Amended) Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to claim 1.

18. (Amended) Host cell according to claim 16, wherein the prokaryotic cell system is E. coli, and the eukaryotic cell system is an animal, human or yeast cell system.

19. (Amended) A process for producing a polypeptide or a fragment, wherein the host cells according to claim 16 are cultivated.

27. (Amended) Use of polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as tools for finding active ingredients against the bladder tumor.

28. (Amended) Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for expression of polypeptides that can be used as tools for finding active ingredients against the bladder tumor.

29. (Amended) Use of nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 in sense or antisense form.

30. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as pharmaceutical agents in gene therapy for treatment of the bladder tumor.

31. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 for the production of a pharmaceutical agent for treatment of the bladder tumor.

32. (Amended) Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431 of claim 23.

33. (Amended) A nucleic acid sequence according to claim 1, wherein it is a genomic sequence.

34. (Amended) A nucleic acid sequence according to claim 1, wherein it is an mRNA sequence.

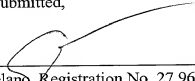
35. (Amended) Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403 of claim 2.

38. (Amended) A nucleic acid sequence according to claim 1, wherein the size of the fragment has a length of at least 300 to 3500 bp.

REMARKS

The purpose of this Preliminary Amendment is to eliminate multiple dependent claims in order to avoid the additional fee. Applicants reserve the right to reintroduce claims to canceled combined subject matter.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

Claims 3-11, 13-14, 16, 18-19, 27-35 and 38 have been amended as follows:

3. (Amended) Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2, characterized in that they are expressed elevated in normal bladder tissue.

4. (Amended) BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for use as vehicles for gene transfer.

5. (Amended) A nucleic acid sequence according to ~~claimsclaim~~ 1-~~to 4~~, wherein it has 90% homology to a human nucleic acid sequence.

6. (Amended) A nucleic acid sequence according to ~~claimsclaim~~ 1-~~to 4~~, wherein it has %~~95~~ homology to a human nucleic acid sequence.

7. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in ~~claimsclaim~~ 1-~~to 6~~, in such a sufficient amount that they hybridize with the sequences according to ~~claimsclaim~~ 1-~~to 6~~.

8. (Amended) A nucleic acid sequence according to ~~claimsclaim~~ 1-~~to 7~~, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. (Amended) A nucleic acid sequence according to ~~claimsclaim~~ 1-~~to 7~~, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. (Amended) A nucleic acid sequence according to ~~one of claimsclaim~~ 1-~~to 9~~, which codes at least one partial sequence of a bioactive polypeptide.

11. (Amended) An expression cassette, comprising a nucleic acid fragment or a sequence according to ~~one of claimsclaim~~ 1-~~to 9~~, together with at least one control or regulatory sequence.

13. (Amended) An expression cassette according to ~~one of claims~~claim 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. (Amended) Use of nucleic acid sequences according to ~~claims~~claim 1 to 10 for producing full-length genes.

16. (Amended) Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to ~~one of claims~~claim 1 to 10.

18. (Amended) Host cell according to ~~one of claims~~claim 16 or 17, wherein the prokaryotic cell system is E. coli, and the eukaryotic cell system is an animal, human or yeast cell system.

19. (Amended) A process for producing a polypeptide or a fragment, wherein the host cells according to claim 16 to 18 are cultivated.

27. (Amended) Use of polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as tools for finding active ingredients against the bladder tumor.

28. (Amended) Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for expression of polypeptides that can be used as tools for finding active ingredients against the bladder tumor.

29. (Amended) Use of nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 in sense or antisense form.

30. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as pharmaceutical agents in gene therapy for treatment of the bladder tumor.

31. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 for the production of a pharmaceutical agent for treatment of the bladder tumor.

32. (Amended) Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431 of claim 23.

33. (Amended) A nucleic acid sequence according to ~~claims~~claim 1-~~to 10~~, wherein it is a genomic sequence.

34. (Amended) A nucleic acid sequence according to ~~claims~~claim 1-~~to 10~~, wherein it is an mRNA sequence.

35. (Amended) Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403 of claim 2.

38. (Amended) A nucleic acid sequence according to ~~claims~~claim 1-~~to 7~~, wherein the size of the fragment has a length of at least 300 to 3500 bp.

Human Nucleic Acid Sequences from Normal Bladder Tissue

The invention relates to human nucleic acid sequences from normal bladder tissue, which code for gene products or portions thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main causes of death by cancer is the bladder tumor, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this possibility of error can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403, which play a role as candidate genes in the bladder tumor, have now been found.

Nucleic acid sequences Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, and 391-403 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a portion thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, and 391-403,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, and 391-403 or a complementary or

allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID Nos. 1-127 and 391-403, which are expressed elevated in the normal bladder tissue.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-127 and 391-403.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-127 and 391-403 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs, ϕ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia),
2. eukaryotic,

such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

Control or regulatory sequences are defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P_R, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as *E. coli* or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides, according to the sequence protocols Seq. ID Nos. 128-390 and 404-431.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq ID Nos. 128-390 and 404-431 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID Nos. 1-127 and 391-403 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The polypeptides of sequences Seq. ID Nos. 128-390 and 404-431 according to the invention can also be used as tools for finding active ingredients against the bladder tumor, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 for expression of polypeptides, which can be used as tools for finding active ingredients against the bladder tumor.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 as pharmaceutical agents in the gene therapy for treatment of bladder tumors or for the production of a pharmaceutical agent for treatment of bladder tumors.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained

from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403, and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences) Seq. ID Nos. 1-127 and 391-403, genomic BAC-, PAC- and cosmid libraries are screened, and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes, and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 for use as vehicles for gene transfer.

Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes)

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus)

Singleton = A contig that contains only one sequence

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins

N = selectively the nucleotide A, T, G or C

X = selectively one of the 20 naturally occurring amino acids

Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

Example 1

Search for Tumor-related Candidate Genes

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

Figures 2b1-2b4 illustrate the lengthening of the bladder tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another.)

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

Example 2

Algorithm for Identification and Lengthening of Partial cDNA Sequences with Altered Expression Pattern

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

2.1 Electronic Northern Blot

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

2.1.1

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 1 was found, which occurs 12.2 x more strongly in the normal bladder tissue than in tumor tissue.

The result is as follows:

Electronic Northern for SEQ. ID NO.: 1

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0312 | 0.0026 | 12.203 | 0.0819 |
| Breast | 0.0064 | 0.0056 | 1.1342 | 0.8817 |
| Small intestine | 0.0092 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0060 | 0.0156 | 0.3838 | 2.6058 |
| Endocrine tissue | 0.0068 | 0.0201 | 0.3396 | 2.9444 |
| Gastrointestinal | 0.0096 | 0.0000 | undef | 0.0000 |
| Brain | 0.0111 | 0.0226 | 0.4909 | 2.0372 |
| Hematopoietic | 0.0107 | 0.0379 | 0.2823 | 3.5422 |
| Skin | 0.0147 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0095 | 0.0000 | undef | 0.0000 |
| Heart | 0.0053 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0173 | 0.0234 | 0.7380 | 1.3551 |
| Lung | 0.0083 | 0.0184 | 0.4516 | 2.2144 |
| Stomach-esophagus | 0.0000 | 0.0230 | 0.0000 | undef |
| Muscle-skeleton | 0.0120 | 0.0120 | 0.9994 | 1.0006 |
| Kidney | 0.0081 | 0.0274 | 0.2974 | 3.3626 |
| Pancreas | 0.0083 | 0.0110 | 0.7479 | 1.3371 |
| Penis | 0.0120 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0044 | 0.0106 | 0.4095 | 2.4423 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0152 | 0.0204 | 0.7482 | 1.3366 |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0096 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0139 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|-----------------------------------------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0083 | Ovary_n | 0.0000 |
| Brain | 0.0063 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0157 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0035 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0107 | Hematopoietic | 0.0171 |
| Lung | 0.0253 | Skin-muscle | 0.0065 |
| Suprarenal gland | 0.0507 | Testicles | 0.0077 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0182 | Nerves | 0.0090 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0377 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0042 |

In an analogous procedure, the following Northernblots were also found:

| Electronic Northern for SEQ. ID NO.: 2 | | | | |
|----------------------------------------|-------------|-------------|--------|--------|
| | NORMAL | TUMOR | Ratios | |
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0741 | 0.0102 | 7.2459 | 0.1380 |
| Breast | 0.0102 | 0.0038 | 2.7221 | 0.3674 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0017 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0038 | 0.0046 | 0.8283 | 1.2072 |
| Brain | 0.0007 | 0.0021 | 0.3600 | 2.7779 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0184 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0032 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0052 | 0.0061 | 0.8467 | 1.1810 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0034 | 0.0060 | 0.5711 | 1.7510 |
| Kidney | 0.0027 | 0.0068 | 0.3965 | 2.5219 |
| Pancreas | 0.0017 | 0.0055 | 0.2991 | 3.3428 |
| Penis | 0.0170 | 0.0267 | 0.4493 | 2.2259 |
| Prostate | 0.0109 | 0.0064 | 1.7060 | 0.5862 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0064 | | | |
| Prostate hyperplasia | 0.0030 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0052 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0278 | Breast | 0.0068 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0061 | Nerves | 0.0010 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0042 |

Electronic Northern for SEQ. ID NO.: 3

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0585 | 0.0153 | 3.8136 | 0.2622 |
| Breast | 0.0064 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0184 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0026 | 0.0000 | undef |
| Endocrine tissue | 0.0204 | 0.0100 | 2.0377 | 0.4907 |
| Gastrointestinal | 0.0077 | 0.0046 | 1.6567 | 0.6036 |
| Brain | 0.0059 | 0.0092 | 0.6400 | 1.5626 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0085 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0173 | 0.0000 | undef | 0.0000 |
| Lung | 0.0104 | 0.0020 | 5.0803 | 0.1968 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0217 | 0.0068 | 3.1722 | 0.3152 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0654 | 0.0362 | 1.8064 | 0.5536 |
| Uterus-endometrium | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0204 | 0.3741 | 2.6732 |
| Uterus-general | 0.0000 | 0.1908 | 0.0000 | undef |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0803 | | | |
| Seminal vesicle | 0.0178 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0106 | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0083 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0128 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0162 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0124 | Lung | 0.0164 |
| Placenta | 0.0000 | Nerves | 0.0050 |
| Prostate | 0.0000 | Prostate | 0.0205 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0333 |

Electronic Northern for SEQ. ID NO.: 4

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0351 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.3000 | 0.0010 | 0.0000 | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 6

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|---------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0390 | 0.0026 | 15.2544 | 0.0656 |
| Breast | 0.0460 | 0.0056 | 8.1663 | 0.1225 |
| Small intestine | 0.0123 | 0.0331 | 0.3707 | 2.6973 |
| Ovary | 0.0000 | 0.0052 | 0.0000 | undef |
| Endocrine tissue | 0.0119 | 0.0050 | 2.3774 | 0.4206 |
| Gastrointestinal | 0.0038 | 0.0000 | undef | 0.0000 |
| Brain | 0.0052 | 0.0072 | 0.7200 | 1.3890 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0294 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0143 | 0.0065 | 2.2059 | 0.4533 |
| Heart | 0.0074 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0117 | 0.4920 | 2.0326 |
| Lung | 0.0021 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0103 | 0.0240 | 0.4283 | 2.3347 |
| Kidney | 0.0516 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0090 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0044 | 0.0064 | 0.6824 | 1.4654 |
| Uterus-endometrium | 0.0270 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0381 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.1087 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0319 | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | | Breast | 0.0272 |
| Gastrointestinal | 0.0557 | Ovary_n | 0.0000 |
| Brain | 0.0028 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0116 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0498 | Skin-muscle | 0.0194 |
| Suprarenal gland | 0.0036 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0151 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0251 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0208 |

Electronic Northern for SEQ. ID NO.: 7

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|---------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0351 | 0.0025 | 13.7290 | 0.0729 |
| Breast | 0.0051 | 0.0038 | 1.3611 | 0.7347 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0060 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0034 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0057 | 0.0046 | 1.2425 | 0.8049 |
| Brain | 0.0044 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0053 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0048 | 0.0000 | undef | 0.0000 |
| Heart | 0.0021 | 0.0137 | 0.1542 | 6.4853 |
| Testicles | 0.0000 | 0.0117 | 0.0000 | undef |
| Lung | 0.0021 | 0.0020 | 1.0161 | 0.9842 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0055 | 0.0000 | undef |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0044 | 0.0021 | 2.0473 | 0.4885 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0035 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0063 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0047 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0063 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0040 |
| Placenta | 0.0061 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0042 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 8

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0234 | 0.0000 | undef | 0.0000 |
| Breast | 0.0013 | 0.0019 | 0.6805 | 1.4694 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0026 | 0.0000 | undef |
| Endocrine tissue | 0.0034 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0022 | 0.0051 | 0.4320 | 2.3149 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0048 | 0.0000 | undef | 0.0000 |
| Heart | 0.0042 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0041 | 0.0000 | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0051 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0017 | 0.0055 | 0.2991 | 3.3428 |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0065 | 0.0043 | 1.5354 | 0.6513 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0026 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0139 | Breast | 0.0068 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0000 | Nerves | 0.0040 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0083 |

Electronic Northern for SEQ. ID NO.: 9

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|---------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0273 | 0.0026 | 10.6781 | 0.0936 |
| Breast | 0.0026 | 0.0019 | 1.3611 | 0.7347 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0060 | 0.0052 | 1.1513 | 0.8686 |
| Endocrine tissue | 0.0051 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0038 | 0.0046 | 0.8283 | 1.2072 |
| Brain | 0.0037 | 0.0051 | 0.7200 | 1.3890 |
| Hematopoietic | 0.0000 | 0.0379 | 0.0000 | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0117 | 0.0000 | undef |
| Lung | 0.0042 | 0.0020 | 2.0321 | 0.4921 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0051 | 0.0060 | 0.8567 | 1.1673 |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0017 | 0.0000 | undef | 0.0000 |
| Penis | 0.0000 | 0.0267 | 0.0000 | undef |
| Prostate | 0.0000 | 0.0085 | 0.0000 | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0030 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0052 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0490 |
| Skin | 0.0000 | Fetal | 0.0017 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0114 |
| Lung | 0.0036 | Skin-muscle | 0.0194 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0061 | Nerves | 0.0040 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 12

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0858 | 0.0358 | 2.3971 | 0.4172 |
| Breast | 0.0435 | 0.0338 | 1.2854 | 0.7779 |
| Small intestine | 0.0276 | 0.0165 | 1.6683 | 0.5994 |
| Ovary | 0.0120 | 0.0182 | 0.6579 | 1.5201 |
| Endocrine tissue | 0.0290 | 0.0176 | 1.6496 | 0.6062 |
| Gastrointestinal | 0.0594 | 0.0231 | 2.5679 | 0.3894 |
| Brain | 0.0333 | 0.0657 | 0.5062 | 1.9754 |
| Hematopoietic | 0.0134 | 0.0000 | undef | 0.0000 |
| Skin | 0.0514 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0381 | 0.0123 | 2.9412 | 0.3400 |
| Heart | 0.0413 | 0.0275 | 1.5034 | 0.6652 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0384 | 0.0164 | 2.3497 | 0.4256 |
| Stomach-esophagus | 0.0290 | 0.0307 | 0.9454 | 1.0578 |
| Muscle-skeleton | 0.0188 | 0.0360 | 0.5235 | 1.9102 |
| Kidney | 0.0217 | 0.0548 | 0.3965 | 2.5219 |
| Pancreas | 0.0132 | 0.0166 | 0.7977 | 1.2536 |
| Penis | 0.0779 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0632 | 0.0447 | 1.4136 | 0.7074 |
| Uterus-endometrium | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0229 | 0.0068 | 3.3668 | 0.2970 |
| Uterus-general | 0.0306 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0416 | | | |
| Prostate hyperplasia | 0.0595 | | | |
| Seminal vesicle | 0.0712 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0087 | | | |
| Cervix | 0.0426 | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.1293 |
| Gastrointestinal | 0.0250 | Ovary_n | 0.1595 |
| Brain | 0.0063 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0118 | Endocrine tissue | 0.0490 |
| Skin | 0.0000 | Fetal | 0.0338 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0000 |
| Lung | 0.0108 | Skin-muscle | 0.0162 |
| Suprarenal gland | 0.1014 | Testicles | 0.0000 |
| Kidney | 0.0185 | Lung | 0.0301 |
| Placenta | 0.0242 | Nerves | 0.0410 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0628 | Sensory Organs | 0.0624 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 13

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0468 | 0.0077 | 6.1018 | 0.1639 |
| Breast | 0.0294 | 0.0075 | 3.9130 | 0.2556 |
| Small intestine | 0.0184 | 0.0165 | 1.1122 | 0.8991 |
| Ovary | 0.0090 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0085 | 0.0050 | 1.6981 | 0.5889 |
| Gastrointestinal | 0.0192 | 0.0000 | undef | 0.0000 |
| Brain | 0.0059 | 0.0062 | 0.9599 | 1.0417 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0808 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0540 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0156 | 0.0082 | 1.9051 | 0.5249 |
| Stomach-esophagus | 0.0193 | 0.0077 | 2.5211 | 0.3967 |
| Muscle-skeleton | 0.1216 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0000 | 0.0274 | 0.0000 | undef |
| Pancreas | 0.0000 | 0.0055 | 0.0000 | undef |
| Penis | 0.1587 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0087 | 0.0106 | 0.8189 | 1.2211 |
| Uterus-endometrium | 0.0338 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0457 | 0.0272 | 1.6834 | 0.5940 |
| Uterus-general | 0.0357 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0160 | | | |
| Prostate hyperplasia | 0.0208 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0009 | | | |
| White blood cells | 0.0426 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0167 |
| Brain | 0.0063 |
| Hematopoietic | 0.0039 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0249 |
| Lung | 0.0108 |
| Suprarenal gland | 0.0254 |
| Kidney | 0.0062 |
| Placenta | 0.0000 |
| Prostate | 0.0249 |
| Sensory organs | 0.0000 |

| | |
|------------------|--------|
| Breast | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0029 |
| Gastrointestinal | 0.0244 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0032 |
| Testicles | 0.0309 |
| Lung | 0.0082 |
| Nerves | 0.0090 |
| Prostate | 0.0000 |
| Sensory Organs | 0.0077 |
| Uterus_n | 0.0208 |

Electronic Northern for SEQ. ID NO.: 14

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|---------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0351 | 0.0026 | 13.7290 | 0.0728 |
| Breast | 0.0102 | 0.0075 | 1.3611 | 0.7347 |
| Small intestine | 0.0092 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0090 | 0.0026 | 3.4538 | 0.2895 |
| Endocrine tissue | 0.0051 | 0.0025 | 2.0377 | 0.4907 |
| Gastrointestinal | 0.0115 | 0.0000 | undef | 0.0000 |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0065 | 0.7353 | 1.3600 |
| Heart | 0.0233 | 0.0137 | 1.6961 | 0.5896 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0135 | 0.0041 | 3.3022 | 0.3028 |
| Stomach-esophagus | 0.0193 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0634 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0027 | 0.0068 | 0.3965 | 2.5219 |
| Pancreas | 0.0017 | 0.0000 | undef | 0.0000 |
| Penis | 0.0359 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0218 | 0.0043 | 5.1181 | 0.1954 |
| Uterus-endometrium | 0.0203 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0229 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0255 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0000 | 0.0000 | | |
| Prostate hyperplasia | 0.0089 | 0.0000 | | |
| Seminal vesicle | 0.0089 | 0.0000 | | |
| Sensory organs | 0.0000 | 0.0000 | | |
| White blood cells | 0.0000 | 0.0000 | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|--------|-------------------------|--------|
| % frequency | | LIBRARIES | |
| | | % frequency | |
| Development | 0.0000 | Breast | 0.0136 |
| Gastrointestinal | 0.0139 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0029 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0244 |
| Heart-blood vessels | 0.0071 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0507 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0181 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0583 |

Electronic Northern for SEQ. ID NO.: 17

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|---------|--------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0273 | 0.0026 | 10.6781 | 0.0936 |
| Breast | 0.0307 | 0.0038 | 8.1663 | 0.1225 |
| Small intestine | 0.0061 | 0.0165 | 0.3707 | 2.6973 |
| Ovary | 0.0030 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0000 | 0.0025 | 0.0000 | undef |
| Gastrointestinal | 0.0249 | 0.0000 | undef | 0.0000 |
| Brain | 0.0015 | 0.0010 | 1.4399 | 0.6945 |
| Hematopoietic | 0.0040 | 0.0000 | undef | 0.0000 |
| Skin | 0.0367 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0148 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0062 | 0.0020 | 3.0482 | 0.3281 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0274 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0050 | 0.0000 | undef | 0.0000 |
| Penis | 0.0120 | 0.0267 | 0.4493 | 2.2259 |
| Prostate | 0.0087 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0229 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0288 | | | |
| Prostate hyperplasia | 0.0030 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0106 | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0111 |
| Brain | 0.0000 |
| Hematopoietic | 0.0039 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0036 |
| Lung | 0.0000 |
| Suprarenal gland | 0.0000 |
| Kidney | 0.0062 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

| | |
|------------------|--------|
| Breast | 0.0204 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0051 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0047 |
| Gastrointestinal | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles | 0.0000 |
| Lung | 0.0000 |
| Nerves | 0.0000 |
| Prostate | 0.0000 |
| Sensory Organs | 0.0083 |
| Uterus_n | |

Electronic Northern for SEQ. ID NO.: 18

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0585 | 0.0230 | 2.5424 | 0.3933 |
| Breast | 0.0013 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0368 | 0.0165 | 2.2244 | 0.4496 |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0051 | 0.0025 | 2.0377 | 0.4907 |
| Gastrointestinal | 0.0115 | 0.0046 | 2.4850 | 0.4024 |
| Brain | 0.0022 | 0.0031 | 0.7200 | 1.3890 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0110 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0095 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0020 | 0.0000 | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0051 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0017 | 0.0000 | undef | undef |
| Pancreas | 0.0509 | 0.0000 | undef | 0.0000 |
| Penis | 0.0218 | 0.0149 | 1.4623 | 0.6838 |
| Prostate | 0.0058 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0229 | 0.0543 | 0.4208 | 2.3761 |
| Uterus-myometrium | 0.0407 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0012 | | | |
| Breast hyperplasia | 0.0059 | | | |
| Prostate hyperplasia | 0.0356 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0106 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES

% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0068 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0052 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0000 |
| Lung | 0.0108 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0030 |
| Placenta | 0.0000 | Nerves | 0.0137 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0083 |
| | | Uterus_n | |

006773646 003604

Electronic Northern for SEQ. ID NO.: 20

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|--------|---------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0429 | 0.0153 | 2.7965 | 0.3576 |
| Breast | 0.0141 | 0.0282 | 0.4991 | 2.0038 |
| Small intestine | 0.0307 | 0.0165 | 1.8537 | 0.5395 |
| Ovary | 0.0300 | 0.0390 | 0.7675 | 1.3029 |
| Endocrine tissue | 0.0409 | 0.0176 | 2.3288 | 0.4294 |
| Gastrointestinal | 0.0230 | 0.0139 | 1.6567 | 0.6036 |
| Brain | 0.0200 | 0.0298 | 0.6703 | 1.4919 |
| Hematopoietic | 0.0160 | 0.0000 | undef | 0.0000 |
| Skin | 0.0257 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0143 | 0.0259 | 0.5515 | 1.8133 |
| Heart | 0.0339 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0288 | 0.0234 | 1.2299 | 0.8130 |
| Lung | 0.0270 | 0.0409 | 0.6604 | 1.5141 |
| Stomach-esophagus | 0.0483 | 0.0230 | 2.1009 | 0.4740 |
| Muscle-skeleton | 0.0394 | 0.0240 | 1.6419 | 0.6090 |
| Kidney | 0.0244 | 0.0205 | 1.1896 | 0.8406 |
| Pancreas | 0.0198 | 0.0276 | 0.7180 | 1.3928 |
| Penis | 0.0359 | 0.0533 | 0.6739 | 1.4839 |
| Prostate | 0.0305 | 0.0255 | 1.1942 | 0.8374 |
| Uterus-endometrium | 0.0270 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0534 | 0.0272 | 1.9640 | 0.5092 |
| Uterus-general | 0.0051 | 0.0954 | 0.0534 | 18.7357 |
| Breast hyperplasia | 0.0384 | | | |
| Prostate hyperplasia | 0.0595 | | | |
| Seminal vesicle | 0.0267 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0286 | | | |
| Cervix | 0.0426 | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0222 | Ovary_n | 0.0000 |
| Brain | 0.0063 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0006 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0244 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0285 | Skin-muscle | 0.0065 |
| Suprarenal gland | 0.0470 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0247 | Nerves | 0.0080 |
| Prostate | 0.0121 | Prostate | 0.0205 |
| Sensory organs | 0.0249 | Sensory Organs | 0.0000 |
| | 0.0377 | Uterus_n | 0.0250 |

Electronic Northern for SEQ. ID NO.: 21

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0195 | 0.0000 | undef | 0.0000 |
| Breast | 0.0026 | 0.0019 | 1.3611 | 0.7347 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0052 | 0.0000 | undef |
| Endocrine tissue | 0.0034 | 0.0150 | 0.2264 | 4.4166 |
| Gastrointestinal | 0.0000 | 0.0139 | 0.0000 | undef |
| Brain | 0.0177 | 0.0031 | 5.7597 | 0.1736 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0000 | undef | 0.0000 |
| Heart | 0.0064 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0117 | 0.0000 | undef |
| Lung | 0.0031 | 0.0123 | 0.2540 | 3.9367 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0027 | 0.0068 | 0.3965 | 2.5219 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0120 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0021 | 0.0000 | undef |
| Uterus-endometrium | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0068 | 1.1223 | 0.8911 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0009 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0142 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0065 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0070 |
| Placenta | 0.0061 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0125 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 22

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0013 | 0.0019 | 0.6805 | 1.4694 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0026 | 0.0000 | undef |
| Endocrine tissue | 0.0017 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0019 | 0.0000 | undef | 0.0000 |
| Brain | 0.0007 | 0.0021 | 0.3600 | 2.7779 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0020 | 0.0000 | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0022 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0132 | 0.0068 | 2.2445 | 0.4453 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0009 | | | |
| Cervix | 0.0000 | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|-----------------------------------------------------|--------|
| Development | 0.0000 | Breast | 0.0136 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0023 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 23

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0390 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0019 | 0.0000 | undef |
| Small intestine | 0.0153 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0030 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0017 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0115 | 0.0046 | 2.4950 | 0.4024 |
| Brain | 0.0022 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0000 | undef | 0.0000 |
| Heart | 0.0021 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0115 | 0.0000 | undef | 0.0000 |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0240 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0065 | 0.0064 | 1.0236 | 0.9769 |
| Uterus-endometrium | 0.0338 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0229 | 0.0475 | 0.4910 | 2.0791 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0149 | | | |
| Prostate hyperplasia | 0.0267 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0106 | | | |
| Cervix | | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0068 |
| Prostate | 0.0249 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 24

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0351 | 0.0051 | 6.8645 | 0.1457 |
| Breast | 0.0026 | 0.0056 | 0.4537 | 2.2042 |
| Small intestine | 0.0092 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0090 | 0.0130 | 0.6908 | 1.4477 |
| Endocrine tissue | 0.0068 | 0.0075 | 0.9057 | 1.1042 |
| Gastrointestinal | 0.0172 | 0.0139 | 1.2425 | 0.8048 |
| Brain | 0.0044 | 0.0092 | 0.5400 | 1.8520 |
| Hematopoietic | 0.0040 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0074 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0173 | 0.0117 | 1.4759 | 0.6775 |
| Lung | 0.0042 | 0.0143 | 0.2903 | 3.4446 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0086 | 0.0060 | 1.4278 | 0.7004 |
| Kidney | 0.0000 | 0.0205 | 0.0000 | undef |
| Pancreas | 0.0033 | 0.0110 | 0.2991 | 3.3428 |
| Penis | 0.0180 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0087 | 0.0128 | 0.6824 | 1.4654 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0102 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0119 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0035 | | | |
| Cervix | 0.0000 | | | |

FETUS
% frequency

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0139 |
| Brain | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0071 |
| Lung | 0.0036 |
| Suprarenal gland | 0.0254 |
| Kidney | 0.0062 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | |
|------------------|--------|
| Breast | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0101 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0181 |
| Gastrointestinal | 0.0000 |
| Hematopoietic | 0.0114 |
| Skin-muscle | 0.0130 |
| Testicles | 0.0154 |
| Lung | 0.0082 |
| Nerves | 0.0060 |
| Prostate | 0.0068 |
| Sensory Organs | 0.0000 |
| Uterus_n | 0.0416 |

Electronic Northern for SEQ. ID NO.: 25

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0234 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 26

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0429 | 0.0000 | undef | 0.0000 |
| Breast | 0.0013 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0030 | 0.0026 | 1.1513 | 0.8686 |
| Endocrine tissue | 0.0034 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0015 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0077 | 0.0000 | undef |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0054 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0090 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0043 | 0.0000 | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0235 | | | |
| Sensory organs | 0.0026 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0245 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0260 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0171 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0042 |
| | | Uterus_n | |

| Electronic Northern for SEQ. ID NO.: 27 | | | | |
|-----------------------------------------|-------------|-------------|--------|--------|
| | NORMAL | TUMOR | Ratios | T/N |
| | % frequency | % frequency | N/T | |
| Bladder | 0.0312 | 0.0000 | undef | 0.0000 |
| Breast | 0.0090 | 0.0056 | 1.5879 | 0.6298 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0060 | 0.0052 | 1.1513 | 0.8686 |
| Endocrine tissue | 0.0034 | 0.0075 | 0.4528 | 2.2083 |
| Gastrointestinal | 0.0077 | 0.0000 | undef | 0.0000 |
| Brain | 0.0030 | 0.0051 | 0.5760 | 1.7362 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0048 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0021 | 0.0000 | undef | 0.0000 |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0010 | 0.0020 | 0.5080 | 1.9684 |
| Lung | 0.0290 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0017 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0054 | 0.0068 | 0.7930 | 1.2610 |
| Kidney | 0.0017 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0090 | 0.0000 | undef | 0.0000 |
| Penis | 0.0065 | 0.0043 | 1.5354 | 0.6513 |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0132 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0059 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0009 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0125 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0245 |
| Skin | 0.0000 | Fetal | 0.0064 |
| Hepatic | 0.0260 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0071 | Hematopoietic | 0.0114 |
| Lung | 0.0000 | Skin-muscle | 0.0065 |
| Suprarenal gland | 0.0000 | Testicles | 0.0154 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0205 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0126 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0167 |

Electronic Northern for SEQ. ID NO.: 29

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|---------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0312 | 0.0051 | 6.1018 | 0.1639 |
| Breast | 0.0307 | 0.0019 | 16.3327 | 0.0612 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0120 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0000 | 0.0075 | 0.0000 | undef |
| Gastrointestinal | 0.0057 | 0.0093 | 0.6213 | 1.6096 |
| Brain | 0.0015 | 0.0062 | 0.2400 | 4.1669 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0147 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0095 | 0.0065 | 1.4706 | 0.6800 |
| Heart | 0.0138 | 0.0412 | 0.3341 | 2.9932 |
| Testicles | 0.0403 | 0.0000 | undef | 0.0000 |
| Lung | 0.0114 | 0.0061 | 1.8628 | 0.5368 |
| Stomach-esophagus | 0.0193 | 0.0153 | 1.2605 | 0.7933 |
| Muscle-skeleton | 0.0274 | 0.0300 | 0.9138 | 1.0944 |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0050 | 0.0331 | 0.1496 | 6.6857 |
| Penis | 0.0359 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0044 | 0.0021 | 2.0473 | 0.4885 |
| Uterus-endometrium | 0.0203 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0686 | 0.0679 | 1.0100 | 0.9901 |
| Uterus-general | 0.0458 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0128 | | | |
| Prostate hyperplasia | 0.0119 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0213 | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0111 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0023 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0097 |
| Suprarenal gland | 0.0000 | Testicles | 0.0077 |
| Kidney | 0.0124 | Lung | 0.0410 |
| Placenta | 0.0061 | Nerves | 0.0000 |
| Prostate | 0.0249 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0250 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 30

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0273 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0030 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0017 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0007 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0021 | 0.0000 | undef | 0.0000 |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0022 | 0.0021 | 1.0236 | 0.9769 |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0059 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0003 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0041 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0010 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0125 |

| Electronic Northern for SEQ. ID NO.: 31 | | | | |
|-----------------------------------------|-------------|-------------|--------|--------|
| | NORMAL | TUMOR | Ratios | |
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0234 | 0.0000 | undef | 0.0000 |
| Breast | 0.0038 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0026 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0053 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0069 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0033 | 0.0055 | 0.5983 | 1.6714 |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0076 | 0.0068 | 1.1223 | 0.8911 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| FETUS | STANDARDIZED/SUBTRACTED | |
|-------------|-------------------------|--------|
| % frequency | LIBRARIES | |
| | % frequency | |
| 0.0000 | Breast | 0.0000 |
| 0.0028 | Ovary_n | 0.0000 |
| 0.0000 | Ovary_t | 0.0000 |
| 0.0000 | Endocrine tissue | 0.0000 |
| 0.0000 | Fetal | 0.0012 |
| 0.0000 | Gastrointestinal | 0.0000 |
| 0.0107 | Hematopoietic | 0.0000 |
| 0.0072 | Skin-muscle | 0.0000 |
| 0.0254 | Testicles | 0.0000 |
| 0.0000 | Lung | 0.0000 |
| 0.0000 | Nerves | 0.0000 |
| 0.0499 | Prostate | 0.0000 |
| 0.0000 | Sensory Organs | 0.0000 |
| | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 32

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0234 | 0.0026 | 9.1527 | 0.1093 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0026 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0050 | 0.0000 | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0007 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0097 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0017 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0052 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0057 |
| Lung | 0.0000 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0121 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0077 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 33

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0195 | 0.0000 | undef | 0.0000 |
| Breast | 0.0013 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0060 | 0.0104 | 0.5756 | 1.7372 |
| Endocrine tissue | 0.0085 | 0.0150 | 0.5660 | 1.7667 |
| Gastrointestinal | 0.0019 | 0.0139 | 0.1391 | 7.2434 |
| Brain | 0.0037 | 0.0010 | 3.5998 | 0.2778 |
| Hematopoietic | 0.0040 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0173 | 0.0117 | 1.4759 | 0.6775 |
| Lung | 0.0042 | 0.0061 | 0.6774 | 1.4763 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0060 | 0.0000 | undef |
| Kidney | 0.0109 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0017 | 0.0000 | undef | 0.0000 |
| Penis | 0.0120 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0021 | 0.0000 | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0026 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0063 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0023 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0130 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0000 | Nerves | 0.0070 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0042 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 34

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0030 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0042 |

Electronic Northern for SEQ. ID NO.: 35

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0013 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0025 | 0.0000 | undef |
| Gastrointestinal | 0.0019 | 0.0046 | 0.4142 | 2.4145 |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0017 | 0.0060 | 0.2856 | 3.5020 |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0035 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0020 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0310 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0042 |
| | | Uterus_n | |

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0195 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|-----------------------------------------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 37

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0038 | 0.0038 | 1.0208 | 0.9796 |
| Small intestine | 0.0184 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0090 | 0.0052 | 1.7269 | 0.5791 |
| Endocrine tissue | 0.0068 | 0.0025 | 2.7170 | 0.3681 |
| Gastrointestinal | 0.0057 | 0.0000 | undef | 0.0000 |
| Brain | 0.0089 | 0.0144 | 0.6171 | 1.6205 |
| Hematopoietic | 0.0040 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0095 | 0.0065 | 1.4706 | 0.6800 |
| Heart | 0.0095 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0115 | 0.0000 | undef | 0.0000 |
| Lung | 0.0135 | 0.0123 | 1.1007 | 0.9085 |
| Stomach-esophagus | 0.0097 | 0.0077 | 1.2605 | 0.7933 |
| Muscle-skeleton | 0.0034 | 0.0120 | 0.2856 | 3.5020 |
| Kidney | 0.0054 | 0.0068 | 0.7930 | 1.2610 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0022 | 0.0149 | 0.1462 | 6.8384 |
| Uterus-endometrium | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0136 | 0.5611 | 1.7821 |
| Uterus-general | 0.0255 | 0.1908 | 0.1334 | 7.4943 |
| Breast hyperplasia | 0.0096 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0104 | | | |
| Cervix | 0.0000 | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.1595 |
| Brain | 0.0000 | Ovary_t | 0.0253 |
| Hematopoietic | 0.0118 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0116 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0366 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0456 |
| Lung | 0.0108 | Skin-muscle | 0.0162 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0221 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0077 |
| | | Uterus_n | 0.0000 |

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0273 | 0.0051 | 5.3391 | 0.1873 |
| Breast | 0.0026 | 0.0075 | 0.3403 | 2.9389 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0030 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0068 | 0.0125 | 0.5434 | 1.8403 |
| Gastrointestinal | 0.0019 | 0.0046 | 0.4142 | 2.4145 |
| Brain | 0.0081 | 0.0031 | 2.6399 | 0.3788 |
| Hematopoietic | 0.0040 | 0.0000 | undef | 0.0000 |
| Skin | 0.0257 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0000 | undef | 0.0000 |
| Heart | 0.0064 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0042 | 0.0102 | 0.4064 | 2.4605 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0069 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0136 | 0.0205 | 0.6609 | 1.5132 |
| Pancreas | 0.0033 | 0.0000 | undef | 0.0000 |
| Penis | 0.0090 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0109 | 0.0021 | 5.1181 | 0.1954 |
| Uterus-endometrium | 0.0068 | 0.0528 | 0.1280 | 7.8106 |
| Uterus-mymometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0128 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | 0.0000 | undef | undef |
| Prostate hyperplasia | 0.0089 | 0.0000 | undef | undef |
| Seminal vesicle | 0.0235 | 0.0000 | undef | undef |
| Sensory organs | 0.0009 | 0.0000 | undef | undef |
| White blood cells | 0.0000 | 0.0000 | undef | undef |
| Cervix | 0.0000 | 0.0000 | undef | undef |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|-----------------------------------------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.0000 |
| Brain | 0.0125 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0107 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0507 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0164 |
| Placenta | 0.0000 | Nerves | 0.0070 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 39

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0195 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0017 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0020 | 0.0000 | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|--------|-------------------------|--------|
| % frequency | | LIBRARIES | |
| | | % frequency | |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 40

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0013 | 0.0019 | 0.6805 | 1.4694 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0026 | 0.0000 | undef |
| Endocrine tissue | 0.0034 | 0.0050 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0057 | 0.0000 | undef | 0.0000 |
| Brain | 0.0007 | 0.0031 | 0.2400 | 4.1669 |
| Hematopoietic | 0.0040 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0058 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0021 | 0.0041 | 0.5080 | 1.9684 |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0086 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0027 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0033 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0051 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0032 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0136 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0035 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0227 |
| Suprarenal gland | 0.0072 | Testicles | 0.0077 |
| Kidney | 0.0254 | Lung | 0.0000 |
| Placenta | 0.0062 | Nerves | 0.0050 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0077 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 43

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0026 | 0.0019 | 1.3611 | 0.7347 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0026 | 0.0000 | undef |
| Endocrine tissue | 0.0017 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0019 | 0.0093 | 0.2071 | 4.8299 |
| Brain | 0.0030 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0032 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0052 | 0.0041 | 1.2701 | 0.7973 |
| Stomach-esophagus | 0.0193 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0069 | 0.0060 | 1.1422 | 0.8755 |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0017 | 0.0055 | 0.2931 | 3.3428 |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0021 | 0.0000 | undef |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0068 | 0.0000 | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0118 | | | |
| Sensory organs | 0.0017 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0152 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0244 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0071 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0036 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0010 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0042 |

Electronic Northern for SEQ. ID NO.: 44

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0195 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 46

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 47

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0273 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0010 | 0.0000 | undef |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0010 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0009 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 48

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0273 | 0.0000 | undef | 0.0000 |
| Breast | 0.0013 | 0.0019 | 0.6805 | 1.4694 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0030 | 0.0052 | 0.5756 | 1.7372 |
| Endocrine tissue | 0.0017 | 0.0025 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0019 | 0.0046 | 0.4142 | 2.4145 |
| Brain | 0.0007 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0000 | undef | 0.0000 |
| Heart | 0.0042 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0010 | 0.0020 | 0.5080 | 1.9684 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0034 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0022 | 0.0021 | 1.0236 | 0.9769 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0068 | 0.0000 | 0.0000 | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0064 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0017 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0278 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0017 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0000 |
| Lung | 0.0072 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0060 |
| Placenta | 0.0061 | Nerves | 0.0000 |
| Prostate | 0.0249 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 50

| | NORMAL | TUMOR | Ratio | |
|----------------------|-------------|-------------|-------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 51
 NORMAL TUMOR Ratios
 % frequency % frequency N/T T/N

| | | | | |
|----------------------|--------|--------|--------|--------|
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0026 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0060 | 0.0078 | 0.7675 | 1.3029 |
| Endocrine tissue | 0.0034 | 0.0025 | 1.3585 | 0.7361 |
| Gastrointestinal | 0.0057 | 0.0000 | undef | 0.0000 |
| Brain | 0.0022 | 0.0021 | 1.0799 | 0.9260 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0053 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0031 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0165 | 0.0000 | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0022 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0032 | | | |
| Breast hyperplasia | 0.0059 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0026 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
 % frequency

STANDARDIZED/SUBTRACTED
 LIBRARIES
 % frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0136 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0041 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0057 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0061 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 52

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0312 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0010 | 0.0000 | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | 0.0000 | undef | undef |
| Prostate hyperplasia | 0.0000 | 0.0000 | undef | undef |
| Seminal vesicle | 0.0000 | 0.0000 | undef | undef |
| Sensory organs | 0.0000 | 0.0000 | undef | undef |
| White blood cells | 0.0000 | 0.0000 | undef | undef |
| Cervix | 0.0000 | 0.0000 | undef | undef |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 53

| | NORMAL | TUMOR | Ratio | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0195 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0010 | 0.0000 | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0027 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0000 | 0.0055 | 0.0000 | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0020 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 54

| | NORMAL % frequency | TUMOR % frequency | Ratio N/T | T/N |
|--|-----------------------|----------------------|--------------|-----|
|--|-----------------------|----------------------|--------------|-----|

| | | | | |
|----------------------|--------|--------|--------|--------|
| Bladder | 0.0195 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0093 | 0.0000 | undef |
| Brain | 0.0000 | 0.0010 | 0.0000 | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0020 | 0.0000 | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0055 | 0.0000 | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0064 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0106 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0037 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 55

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0234 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0077 | 0.0000 | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES % frequency | |
|---------------------|----------------------|-----------------------------------------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 56

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0026 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0030 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0051 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0038 | 0.0093 | 0.4142 | 2.4145 |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0010 | 0.0020 | 0.5080 | 1.9684 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0054 | 0.0068 | 0.7930 | 1.2610 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0022 | 0.0043 | 0.5118 | 1.9538 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0030 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0009 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|--------|-------------------------|--------|
| % frequency | | LIBRARIES | |
| | | % frequency | |
| Development | 0.0000 | Breast | 0.0136 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0228 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0000 | Nerves | 0.0040 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0083 |

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0025 | 0.0000 | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0007 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0010 | 0.0041 | 0.2540 | 3.9367 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0055 | 0.0000 | undef |
| Penis | 0.0000 | 0.0267 | 0.0000 | undef |
| Prostate | 0.0065 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0058 | 0.0000 | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0030 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0077 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 58
 NORMAL TUMOR Ratios
 % frequency % frequency N/T T/N

| | | | | |
|----------------------|--------|--------|--------|--------|
| Bladder | 0.0234 | 0.0026 | 9.1527 | 0.1093 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
 % frequency

STANDARDIZED/SUBTRACTED
 LIBRARIES
 % frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 59

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0273 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0117 | 0.0000 | undef |
| Testicles | 0.0000 | 0.0020 | 0.0000 | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 60

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0051 | 0.0038 | 1.3611 | 0.7347 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0030 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0051 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0038 | 0.0000 | undef | 0.0000 |
| Brain | 0.0022 | 0.0021 | 1.0799 | 0.9260 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0021 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0060 | 0.0000 | undef |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0050 | 0.0000 | undef | 0.0000 |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0021 | 0.0000 | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0009 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.1595 |
| Brain | 0.0000 | Ovary_t | 0.0203 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0070 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 61

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|---------------|-----|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0156 | 0.0000 | undef 0.0000 | |
| Breast | 0.0000 | 0.0000 | undef undef | |
| Small intestine | 0.0061 | 0.0165 | 0.3707 2.6973 | |
| Ovary | 0.0030 | 0.0052 | 0.5756 1.7372 | |
| Endocrine tissue | 0.0034 | 0.0075 | 0.4528 2.2083 | |
| Gastrointestinal | 0.0000 | 0.0046 | 0.0000 undef | |
| Brain | 0.0067 | 0.0051 | 1.2959 0.7716 | |
| Hematopoietic | 0.0000 | 0.0000 | undef undef | |
| Skin | 0.0000 | 0.0000 | undef undef | |
| Hepatic | 0.0000 | 0.0000 | undef undef | |
| Heart | 0.0074 | 0.0000 | undef 0.0000 | |
| Testicles | 0.0000 | 0.0117 | 0.0000 undef | |
| Lung | 0.0031 | 0.0061 | 0.5080 1.9684 | |
| Stomach-esophagus | 0.0097 | 0.0077 | 1.2605 0.7933 | |
| Muscle-skeleton | 0.0034 | 0.0120 | 0.2856 3.5020 | |
| Kidney | 0.0081 | 0.0068 | 1.1896 0.8406 | |
| Pancreas | 0.0066 | 0.0000 | undef 0.0000 | |
| Penis | 0.0060 | 0.0000 | undef 0.0000 | |
| Prostate | 0.0000 | 0.0000 | undef undef | |
| Uterus-endometrium | 0.0000 | 0.0068 | 0.0000 undef | |
| Uterus-myometrium | 0.0153 | 0.0000 | undef 0.0000 | |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0030 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0061 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0152 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0064 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0130 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0002 |
| Placenta | 0.0000 | Nerves | 0.0010 |
| Prostate | 0.0249 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0042 |

Electronic Northern for SEQ. ID NO.: 62

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0030 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0019 | 0.0000 | undef | 0.0000 |
| Brain | 0.0022 | 0.0010 | 2.1599 | 0.4630 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0043 | 0.0000 | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0068 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0063 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0006 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 63

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0351 | 0.0051 | 6.8645 | 0.1457 |
| Breast | 0.0026 | 0.0075 | 0.3403 | 2.9389 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0052 | 0.0000 | undef |
| Endocrine tissue | 0.0034 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0019 | 0.0046 | 0.4142 | 2.4145 |
| Brain | 0.0015 | 0.0041 | 0.3600 | 2.7779 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0000 | undef | 0.0000 |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0058 | 0.0117 | 0.4920 | 2.0326 |
| Lung | 0.0042 | 0.0041 | 1.0161 | 0.9842 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0120 | 0.0000 | undef |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0017 | 0.0000 | undef | 0.0000 |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0022 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0089 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0118 | | | |
| Sensory organs | 0.0009 | | | |
| White blood cells | 0.0106 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0278 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0012 |
| Skin | 0.0000 | Fetal | 0.0122 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0097 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0050 |
| Placenta | 0.0061 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0042 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 65

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0195 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | 0.0000 | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | 0.0000 |
| Penis | 0.0030 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0077 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 67

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0390 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0017 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0235 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0245 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0037 |
| Lung | 0.0036 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 69

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|---------|---------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0858 | 0.0077 | 11.1866 | 0.0894 |
| Breast | 0.0102 | 0.0075 | 1.3611 | 0.7347 |
| Small intestine | 0.0092 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0060 | 0.0260 | 0.2303 | 4.3431 |
| Endocrine tissue | 0.0068 | 0.0125 | 0.5434 | 1.8403 |
| Gastrointestinal | 0.0038 | 0.0278 | 0.1381 | 7.2434 |
| Brain | 0.0022 | 0.0144 | 0.1543 | 6.4818 |
| Hematopoietic | 0.0013 | 0.0379 | 0.0353 | 28.3379 |
| Skin | 0.0734 | 0.1695 | 0.4332 | 2.3084 |
| Hepatic | 0.0000 | 0.0194 | 0.0000 | undef |
| Heart | 0.0159 | 0.0137 | 1.1565 | 0.8647 |
| Testicles | 0.0000 | 0.0468 | 0.0000 | undef |
| Lung | 0.0073 | 0.0164 | 0.4445 | 2.2496 |
| Stomach-esophagus | 0.0000 | 0.0230 | 0.0000 | undef |
| Muscle-skeleton | 0.0069 | 0.0180 | 0.3807 | 2.6265 |
| Kidney | 0.0163 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0066 | 0.0055 | 1.1966 | 0.8357 |
| Penis | 0.0210 | 0.0267 | 0.7862 | 1.2719 |
| Prostate | 0.0044 | 0.0021 | 2.0473 | 0.4885 |
| Uterus-endometrium | 0.0338 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0068 | 1.1223 | 0.8911 |
| Uterus-general | 0.0255 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0128 | | | |
| Prostate hyperplasia | 0.0119 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0235 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0000 | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0245 |
| Skin | 0.0000 | Fetal | 0.0128 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0462 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0227 |
| Suprarenal gland | 0.0000 | Testicles | 0.0154 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0171 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0155 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 72

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|---------------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0585 | 0.0077 | 7.6272 0.1311 | |
| Breast | 0.0192 | 0.0019 | 10.2079 | 0.0980 |
| Small intestine | 0.0123 | 0.0000 | undef 0.0000 | |
| Ovary | 0.0090 | 0.0052 | 1.7269 0.5791 | |
| Endocrine tissue | 0.0000 | 0.0075 | 0.0000 undef | |
| Gastrointestinal | 0.0307 | 0.0000 | undef 0.0000 | |
| Brain | 0.0118 | 0.0062 | 1.9199 0.5209 | |
| Hematopoietic | 0.0013 | 0.0000 | undef 0.0000 | |
| Skin | 0.0184 | 0.0000 | undef 0.0000 | |
| Hepatic | 0.0190 | 0.0065 | 2.9412 0.3400 | |
| Heart | 0.0244 | 0.0000 | undef 0.0000 | |
| Testicles | 0.0058 | 0.0000 | undef 0.0000 | |
| Lung | 0.0010 | 0.0041 | 0.2540 3.9367 | |
| Stomach-esophagus | 0.0000 | 0.0077 | 0.0000 undef | |
| Muscle-skeleton | 0.0086 | 0.0000 | undef 0.0000 | |
| Kidney | 0.0054 | 0.0000 | undef 0.0000 | |
| Pancreas | 0.0033 | 0.0000 | undef 0.0000 | |
| Penis | 0.0509 | 0.0000 | undef 0.0000 | |
| Prostate | 0.0153 | 0.0085 | 1.7913 0.5582 | |
| Uterus-endometrium | 0.0135 | 0.0000 | undef 0.0000 | |
| Uterus-myometrium | 0.0152 | 0.0000 | undef 0.0000 | |
| Uterus-general | 0.0102 | 0.0000 | undef 0.0000 | |
| Breast hyperplasia | 0.0320 | | | |
| Prostate hyperplasia | 0.0238 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0000 | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0204 |
| Gastrointestinal | 0.0167 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0082 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0071 | Hematopoietic | 0.0162 |
| Lung | 0.0036 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0082 |
| Kidney | 0.0000 | Lung | 0.0040 |
| Placenta | 0.0061 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0155 |
| Sensory organs | 0.0251 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 73

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0013 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0007 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 75

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0013 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0025 | 0.0000 | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0010 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0009 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0037 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 77

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0351 | 0.0051 | 6.8645 | 0.1457 |
| Breast | 0.0026 | 0.0019 | 1.3611 | 0.7347 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0104 | 0.0000 | undef |
| Endocrine tissue | 0.0034 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0019 | 0.0093 | 0.2071 | 4.8289 |
| Brain | 0.0067 | 0.0010 | 6.4796 | 0.1543 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0095 | 0.0000 | undef | 0.0000 |
| Heart | 0.0117 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0010 | 0.0041 | 0.2540 | 3.9367 |
| Stomach-esophagus | 0.0097 | 0.0077 | 1.2605 | 0.7933 |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0054 | 0.0137 | 0.3965 | 2.5213 |
| Pancreas | 0.0017 | 0.0000 | undef | 0.0000 |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0229 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0030 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0035 | | | |
| Cervix | 0.0000 | | | |

| FETUS | STANDARDIZED/SUBTRACTED | |
|-------------|-------------------------|--------|
| % frequency | LIBRARIES | |
| | % frequency | |
| | Breast | 0.0000 |
| 0.0000 | Ovary_n | 0.0000 |
| 0.0056 | Ovary_t | 0.0100 |
| 0.0000 | Endocrine tissue | 0.0000 |
| 0.0000 | Fetal | 0.0080 |
| 0.0000 | Gastrointestinal | 0.0000 |
| 0.0000 | Hematopoietic | 0.0050 |
| 0.0000 | Skin-muscle | 0.0130 |
| 0.0072 | Testicles | 0.0000 |
| 0.0000 | Lung | 0.0090 |
| 0.0000 | Nerves | 0.0060 |
| 0.0000 | Prostate | 0.0000 |
| 0.0000 | Sensory Organs | 0.0450 |
| 0.0000 | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 78

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|---------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0093 | 0.0000 | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0011 | 0.0412 | 0.0257 | 38.9118 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0020 | 0.0000 | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0278 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 79

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0351 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS % frequency | STANDARDIZED/SUBTRACTED LIBRARIES | |
|---------------------|----------------------|--------------------------------------|--------|
| | | % frequency | |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 80

| | NORMAL | TUMOR | Ratio | T/N |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0624 | 0.0102 | 6.1018 | 0.1639 |
| Breast | 0.0141 | 0.0056 | 2.4953 | 0.4008 |
| Small intestine | 0.0215 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0150 | 0.0078 | 1.9188 | 0.5212 |
| Endocrine tissue | 0.0187 | 0.0050 | 3.7359 | 0.2677 |
| Gastrointestinal | 0.0307 | 0.0139 | 2.2089 | 0.4527 |
| Brain | 0.0214 | 0.0082 | 2.6099 | 0.3832 |
| Hematopoietic | 0.0053 | 0.0000 | undef | 0.0000 |
| Skin | 0.0147 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0190 | 0.0065 | 2.9412 | 0.3400 |
| Heart | 0.0360 | 0.0137 | 2.6213 | 0.3815 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0083 | 0.0041 | 2.0321 | 0.4921 |
| Stomach-esophagus | 0.0097 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0171 | 0.0060 | 2.8555 | 0.3502 |
| Kidney | 0.0136 | 0.0548 | 0.2478 | 4.0351 |
| Pancreas | 0.0083 | 0.0387 | 0.2137 | 4.6800 |
| Penis | 0.0150 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0087 | 0.0064 | 1.3648 | 0.7327 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0255 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0288 | | | |
| Prostate hyperplasia | 0.0119 | | | |
| Seminal vesicle | 0.1246 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0017 | | | |
| Cervix | 0.0000 | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0136 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0000 |
| Lung | 0.0108 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0077 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0000 | Nerves | 0.0010 |
| Prostate | 0.0000 | Prostate | 0.0205 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0083 |

Electronic Northern for SEQ. ID NO.: 82

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0390 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0017 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | 0.0000 |
| Heart | 0.0011 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | | Sensory Organs | 0.0000 |
| | | Uterus_n | |

| | NORMAL | TUMOR | Ratios | |
|--|-------------|-------------|--------|-----|
| | % frequency | % frequency | N/T | T/N |

| | |
|-------------|-------------------------|
| FETUS | STANDARDIZED/SUBTRACTED |
| % frequency | LIBRARIES |
| | % frequency |

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0068 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0253 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0006 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0201 |
| Placenta | 0.0061 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0310 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 85

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0000 | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 86

| | NORMAL | TUMOR | Ratios | |
|--|-------------|-------------|--------|-----|
| | % frequency | % frequency | N/T | T/N |

| | | | | |
|----------------------|--------|--------|--------|--------|
| Bladder | 0.0273 | 0.0051 | 5.3391 | 0.1873 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0017 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0013 | 0.0000 | undef | 0.0000 |
| Brain | 0.0000 | 0.0010 | 0.0000 | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0021 | 0.0041 | 0.5080 | 1.9684 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0060 | 0.0000 | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0044 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0009 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 88

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0030 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0051 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0007 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0021 | 0.0020 | 1.0161 | 0.9842 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0022 | 0.0043 | 0.5118 | 1.9538 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0009 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | 0.0000 | Breast | 0.0068 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0052 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0386 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0208 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 90

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0312 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0015 | 0.0010 | 1.4399 | 0.6945 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0006 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0010 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 92

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0312 | 0.0051 | 6.1018 | 0.1639 |
| Breast | 0.0102 | 0.0113 | 0.9074 | 1.1021 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0030 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0051 | 0.0125 | 0.4075 | 2.4537 |
| Gastrointestinal | 0.0077 | 0.0000 | undef | 0.0000 |
| Brain | 0.0067 | 0.0329 | 0.2025 | 4.9386 |
| Hematopoietic | 0.0080 | 0.0000 | undef | 0.0000 |
| Skin | 0.0330 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0333 | 0.0323 | 1.0294 | 0.9714 |
| Heart | 0.0127 | 0.0137 | 0.9252 | 1.0809 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0156 | 0.0082 | 1.9051 | 0.5249 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0051 | 0.0120 | 0.4283 | 2.3347 |
| Kidney | 0.0027 | 0.0205 | 0.1322 | 7.5658 |
| Pancreas | 0.0050 | 0.0110 | 0.4487 | 2.2286 |
| Penis | 0.0060 | 0.0267 | 0.2246 | 4.4517 |
| Prostate | 0.0131 | 0.0128 | 1.0236 | 0.9769 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0102 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0128 | | | |
| Prostate hyperplasia | 0.0208 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0147 | | | |
| Cervix | 0.0000 | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | % frequency | |
| Development | 0.0000 | Breast | 0.0340 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0608 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0198 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0171 |
| Lung | 0.0072 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0020 |
| Placenta | 0.0545 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0697 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 93

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0234 | 0.0000 | undef | 0.0000 |
| Breast | 0.0166 | 0.0226 | 0.7372 | 1.3564 |
| Small intestine | 0.0000 | 0.0165 | 0.0000 | undef |
| Ovary | 0.0270 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0238 | 0.0276 | 0.8645 | 1.1567 |
| Gastrointestinal | 0.0115 | 0.0093 | 1.2425 | 0.8048 |
| Brain | 0.0089 | 0.0072 | 1.2342 | 0.8102 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0220 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0143 | 0.0518 | 0.2757 | 3.6266 |
| Heart | 0.0148 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0230 | 0.0117 | 1.9679 | 0.5082 |
| Lung | 0.0218 | 0.0266 | 0.8207 | 1.2185 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0120 | 0.0120 | 0.9994 | 1.0006 |
| Kidney | 0.0081 | 0.0137 | 0.5948 | 1.6813 |
| Pancreas | 0.0149 | 0.0221 | 0.6731 | 1.4857 |
| Penis | 0.0180 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0240 | 0.0213 | 1.1260 | 0.8881 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0229 | 0.0340 | 0.6734 | 1.4851 |
| Uterus-general | 0.0204 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0224 | | | |
| Prostate hyperplasia | 0.0208 | | | |
| Seminal vesicle | 0.0445 | | | |
| Sensory organs | 0.0235 | | | |
| White blood cells | 0.0009 | | | |
| Cervix | 0.0213 | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0167 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0245 |
| Skin | 0.0000 | Fetal | 0.0099 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0065 |
| Lung | 0.0108 | Skin-muscle | 0.0154 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0020 |
| Placenta | 0.0061 | Nerves | 0.0068 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0042 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 94

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0195 | 0.0026 | 7.6272 | 0.1311 |
| Breast | 0.0051 | 0.0094 | 0.5444 | 1.8368 |
| Small intestine | 0.0092 | 0.0165 | 0.5561 | 1.7982 |
| Ovary | 0.0000 | 0.0052 | 0.0000 | undef |
| Endocrine tissue | 0.0119 | 0.0150 | 0.7925 | 1.2619 |
| Gastrointestinal | 0.0019 | 0.0000 | undef | 0.0000 |
| Brain | 0.0030 | 0.0103 | 0.2890 | 3.4724 |
| Hematopoietic | 0.0067 | 0.0000 | undef | 0.0000 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0032 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0052 | 0.0020 | 2.5402 | 0.3937 |
| Stomach-esophagus | 0.0000 | 0.0153 | 0.0000 | undef |
| Muscle-skeleton | 0.0017 | 0.0120 | 0.1428 | 7.0040 |
| Kidney | 0.0081 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0050 | 0.0055 | 0.8974 | 1.1143 |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0022 | 0.0043 | 0.5118 | 1.9538 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0381 | 0.0068 | 5.6113 | 0.1782 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0096 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0095 | | | |
| White blood cells | 0.0106 | | | |
| Cervix | | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0000 | Breast | 0.0204 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0709 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.2513 | Fetal | 0.0070 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0228 |
| Lung | 0.0036 | Skin-muscle | 0.0194 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0185 | Lung | 0.0010 |
| Placenta | 0.0061 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0250 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 95

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0351 | 0.0026 | 13.7290 | 0.0729 |
| Breast | 0.0026 | 0.0094 | 0.2722 | 3.6736 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0026 | 0.0000 | undef |
| Endocrine tissue | 0.0000 | 0.0075 | 0.0000 | undef |
| Gastrointestinal | 0.0000 | 0.0093 | 0.0000 | undef |
| Brain | 0.0037 | 0.0051 | 0.7200 | 1.3890 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0190 | 0.0129 | 1.4706 | 0.6800 |
| Heart | 0.0064 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0117 | 0.4920 | 2.0326 |
| Lung | 0.0021 | 0.0061 | 0.3387 | 2.9526 |
| Stomach-esophagus | 0.0000 | 0.0077 | 0.0000 | undef |
| Muscle-skeleton | 0.0000 | 0.0060 | 0.0000 | undef |
| Kidney | 0.0081 | 0.0068 | 1.1896 | 0.8406 |
| Pancreas | 0.0050 | 0.0166 | 0.2991 | 3.3428 |
| Penis | 0.0060 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0044 | 0.0106 | 0.4095 | 2.4423 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0068 | 0.0000 | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0061 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0063 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0116 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0016 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0194 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0082 |
| Placenta | 0.0000 | Nerves | 0.0010 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0251 | Sensory Organs | 0.0155 |
| | | Uterus_n | 0.0208 |

Electronic Northern for SEQ. ID NO.: 96

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0195 | 0.0000 | undef | 0.0000 |
| Breast | 0.0090 | 0.0094 | 0.9527 | 1.0496 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0153 | 0.0176 | 0.8733 | 1.1451 |
| Gastrointestinal | 0.0096 | 0.0185 | 0.5177 | 1.9316 |
| Brain | 0.0081 | 0.0031 | 2.6399 | 0.3789 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0095 | 0.0000 | undef | 0.0000 |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0052 | 0.0020 | 2.5402 | 0.3937 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0054 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0050 | 0.0055 | 0.8974 | 1.1143 |
| Penis | 0.0180 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0022 | 0.0064 | 0.3412 | 2.9308 |
| Uterus-endometrium | 0.0135 | 0.0528 | 0.2561 | 3.9053 |
| Uterus-myometrium | 0.0076 | 0.0136 | 0.5611 | 1.7821 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0083 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0099 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0071 | Hematopoietic | 0.0000 |
| Lung | 0.0072 | Skin-muscle | 0.0324 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0328 |
| Placenta | 0.0061 | Nerves | 0.0141 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0251 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0167 |

Electronic Northern for SEQ. ID NO.: 97

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0195 | 0.0000 | undef | 0.0000 |
| Breast | 0.0064 | 0.0038 | 1.7013 | 0.5878 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0030 | 0.0156 | 0.1919 | 5.2117 |
| Endocrine tissue | 0.0136 | 0.0251 | 0.5434 | 1.8403 |
| Gastrointestinal | 0.0134 | 0.0139 | 0.9664 | 1.0348 |
| Brain | 0.0074 | 0.0277 | 0.2667 | 3.7502 |
| Hematopoietic | 0.0134 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0065 | 0.7353 | 1.3600 |
| Heart | 0.0127 | 0.0412 | 0.3084 | 3.2426 |
| Testicles | 0.0115 | 0.0585 | 0.1968 | 5.0816 |
| Lung | 0.0104 | 0.0204 | 0.5080 | 1.9684 |
| Stomach-esophagus | 0.0193 | 0.0230 | 0.8404 | 1.1900 |
| Muscle-skeleton | 0.0120 | 0.0240 | 0.4997 | 2.0011 |
| Kidney | 0.0054 | 0.0068 | 0.7930 | 1.2610 |
| Pancreas | 0.0083 | 0.0331 | 0.2493 | 4.0114 |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0240 | 0.0277 | 0.8661 | 1.1545 |
| Uterus-endometrium | 0.0000 | 0.1055 | 0.0000 | undef |
| Uterus-myometrium | 0.0152 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0153 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0064 | 0.0178 | | |
| Prostate hyperplasia | 0.0078 | 0.0089 | | |
| Seminal vesicle | 0.0000 | 0.0000 | | |
| Sensory organs | 0.0113 | 0.0000 | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0111 |
| Brain | 0.0000 |
| Hematopoietic | 0.0039 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0036 |
| Lung | 0.0181 |
| Suprarenal gland | 0.0000 |
| Kidney | 0.0124 |
| Placenta | 0.0000 |
| Prostate | 0.0249 |
| Sensory organs | 0.0000 |

| | |
|------------------|--------|
| Breast | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0051 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0012 |
| Gastrointestinal | 0.0122 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0065 |
| Testicles | 0.0000 |
| Lung | 0.0082 |
| Nerves | 0.0070 |
| Prostate | 0.0068 |
| Sensory Organs | 0.0000 |
| Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 98

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|----------------|-----|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0156 | 0.0000 | undef 0.0000 | |
| Breast | 0.0026 | 0.0113 | 0.2258 4.4083 | |
| Small intestine | 0.0031 | 0.0000 | undef 0.0000 | |
| Ovary | 0.0060 | 0.0026 | 2.3025 0.4343 | |
| Endocrine tissue | 0.0119 | 0.0100 | 1.1887 0.8413 | |
| Gastrointestinal | 0.0077 | 0.0000 | undef 0.0000 | |
| Brain | 0.0229 | 0.0062 | 3.7199 0.2688 | |
| Hematopoietic | 0.0027 | 0.0000 | undef 0.0000 | |
| Skin | 0.0000 | 0.0847 | 0.0000 undef | |
| Hepatic | 0.0095 | 0.0000 | undef 0.0000 | |
| Heart | 0.0032 | 0.0000 | undef 0.0000 | |
| Testicles | 0.0115 | 0.0000 | undef 0.0000 | |
| Lung | 0.0062 | 0.0041 | 1.5241 0.6561 | |
| Stomach-esophagus | 0.0000 | 0.0000 | undef undef | |
| Muscle-skeleton | 0.0000 | 0.0000 | undef undef | |
| Kidney | 0.0027 | 0.0137 | 0.1983 5.0439 | |
| Pancreas | 0.0033 | 0.0055 | 0.5983 1.6714 | |
| Penis | 0.0090 | 0.0000 | undef 0.0000 | |
| Prostate | 0.0044 | 0.0064 | 0.6824 1.4654 | |
| Uterus-endometrium | 0.0000 | 0.0528 | 0.0000 undef | |
| Uterus-myometrium | 0.0000 | 0.0136 | 0.0000 undef | |
| Uterus-general | 0.0051 | 0.0954 | 0.0534 18.7357 | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0061 | | | |
| White blood cells | 0.0106 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0557 | Breast | 0.0068 |
| Gastrointestinal | 0.0083 | Ovary_n | 0.0000 |
| Brain | 0.0188 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0245 |
| Skin | 0.0000 | Fetal | 0.0175 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0142 | Hematopoietic | 0.0114 |
| Lung | 0.0000 | Skin-muscle | 0.0389 |
| Suprarenal gland | 0.0254 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0164 |
| Placenta | 0.0000 | Nerves | 0.0251 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0251 | Sensory Organs | 0.0310 |
| | | Uterus_n | 0.0209 |

Electronic Northern for SEQ. ID NO.: 99

| | NORMAL % frequency | TUMOR % frequency | Ratios N/T | T/N |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder | 0.0312 | 0.0026 | 12.2035 | 0.0819 |
| Breast | 0.0166 | 0.0132 | 1.2638 | 0.7912 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0090 | 0.0026 | 3.4538 | 0.2895 |
| Endocrine tissue | 0.0085 | 0.0025 | 3.3962 | 0.2944 |
| Gastrointestinal | 0.0115 | 0.0231 | 0.4970 | 2.0121 |
| Brain | 0.0074 | 0.0082 | 0.8999 | 1.1112 |
| Hematopoietic | 0.0120 | 0.0379 | 0.3176 | 3.1487 |
| Skin | 0.0147 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0085 | 0.0275 | 0.3084 | 3.2426 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0104 | 0.0061 | 1.6934 | 0.5905 |
| Stomach-esophagus | 0.0193 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0051 | 0.0180 | 0.2856 | 3.5020 |
| Kidney | 0.0109 | 0.0274 | 0.3965 | 2.5219 |
| Pancreas | 0.0017 | 0.0000 | undef | 0.0000 |
| Penis | 0.0150 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0022 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0203 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0255 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0224 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0113 | | | |
| Cervix | 0.0106 | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0111 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0035 |
| Hepatic | 0.0260 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0107 | Hematopoietic | 0.0057 |
| Lung | 0.0036 | Skin-muscle | 0.0130 |
| Suprarenal gland | 0.0507 | Testicles | 0.0000 |
| Kidney | 0.0247 | Lung | 0.0000 |
| Placenta | 0.0061 | Nerves | 0.0040 |
| Prostate | 0.0000 | Prostate | 0.0205 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0042 |

Electronic Northern for SEQ. ID NO.: 100

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|---------------|-----|
| | % frequency | % frequency | N/T | |
| Bladder | | | | |
| Breast | 0.0156 | 0.0000 | undef 0.0000 | |
| Small intestine | 0.0031 | 0.0056 | 0.9074 1.1021 | |
| Ovary | 0.0000 | 0.0000 | undef undef | |
| Endocrine tissue | 0.0030 | 0.0026 | 1.1513 0.8686 | |
| Gastrointestinal | 0.0000 | 0.0075 | 0.0000 undef | |
| Brain | 0.0000 | 0.0000 | undef undef | |
| Hematopoietic | 0.0030 | 0.0051 | 0.5760 1.7362 | |
| Skin | 0.0013 | 0.0000 | undef 0.0000 | |
| Hepatic | 0.0000 | 0.0000 | undef undef | |
| Heart | 0.0021 | 0.0137 | 0.1542 6.4853 | |
| Testicles | 0.0058 | 0.0000 | undef 0.0000 | |
| Lung | 0.0052 | 0.0041 | 1.2701 0.7873 | |
| Stomach-esophagus | 0.0000 | 0.0000 | undef undef | |
| Muscle-skeleton | 0.0034 | 0.0000 | undef 0.0000 | |
| Kidney | 0.0027 | 0.0000 | undef 0.0000 | |
| Pancreas | 0.0000 | 0.0055 | 0.0000 undef | |
| Penis | 0.0060 | 0.0000 | undef 0.0000 | |
| Prostate | 0.0044 | 0.0000 | undef 0.0000 | |
| Uterus-endometrium | 0.0000 | 0.0000 | undef undef | |
| Uterus-myometrium | 0.0000 | 0.0136 | 0.0000 undef | |
| Uterus-general | 0.0000 | 0.0000 | undef undef | |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0061 | | | |
| Cervix | 0.0000 | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

Development 0.0000
Gastrointestinal 0.0000
Brain 0.0000
Hematopoietic 0.0000
Skin 0.0000
Hepatic 0.0000
Heart-blood vessels 0.0000
Lung 0.0000
Suprarenal gland 0.0000
Kidney 0.0000
Placenta 0.0000
Prostate 0.0000
Sensory organs 0.0000

Breast 0.0068
Ovary_n 0.0000
Ovary_t 0.0000
Endocrine tissue 0.0000
Fetal 0.0006
Gastrointestinal 0.0122
Hematopoietic 0.0000
Skin-muscle 0.0065
Testicles 0.0000
Lung 0.0030
Nerves 0.0000
Prostate 0.0000
Sensory Organs 0.0125
Uterus_n 0.0125

Electronic Northern for SEQ. ID NO.: 101

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0234 | 0.0026 | 9.1527 | 0.1093 |
| Breast | 0.0077 | 0.0094 | 0.8165 | 1.2245 |
| Small intestine | 0.0123 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0060 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0034 | 0.0050 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0057 | 0.0139 | 0.4142 | 2.4145 |
| Brain | 0.0015 | 0.0021 | 0.7200 | 1.3890 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0048 | 0.0129 | 0.3676 | 2.7200 |
| Heart | 0.0074 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0052 | 0.0020 | 2.5402 | 0.3937 |
| Stomach-esophagus | 0.0097 | 0.0077 | 1.2605 | 0.7933 |
| Muscle-skeleton | 0.0069 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0081 | 0.0137 | 0.5948 | 1.6813 |
| Pancreas | 0.0000 | 0.0166 | 0.0000 | undef |
| Penis | 0.0150 | 0.0800 | 0.1872 | 5.3421 |
| Prostate | 0.0109 | 0.0085 | 1.2795 | 0.7815 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0102 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0064 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0113 | | | |
| White blood cells | 0.0078 | | | |
| Cervix | 0.0213 | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0000 | Breast | 0.0408 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.1595 |
| Brain | 0.0000 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Petal | 0.0029 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0108 | Skin-muscle | 0.0130 |
| Suprarenal gland | 0.0000 | Testicles | 0.0154 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 102

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0026 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0025 | 0.0000 | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0015 | 0.0010 | 1.4399 | 0.6945 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0021 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0017 | 0.0000 | undef | 0.0000 |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0065 | 0.0021 | 3.0709 | 0.3256 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0102 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0030 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0204 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0070 |
| Hepatic | 0.0260 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0137 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 103

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0019 | 0.0000 | undef | 0.0000 |
| Brain | 0.0000 | 0.0000 | undef | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 104

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|--------|---------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0312 | 0.0051 | 6.1018 | 0.1639 |
| Breast | 0.0102 | 0.0056 | 1.8147 | 0.5510 |
| Small intestine | 0.0092 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0180 | 0.0104 | 1.7269 | 0.5791 |
| Endocrine tissue | 0.0085 | 0.0176 | 0.4852 | 2.0611 |
| Gastrointestinal | 0.0172 | 0.0046 | 3.7275 | 0.2683 |
| Brain | 0.0126 | 0.0123 | 1.0199 | 0.9804 |
| Hematopoietic | 0.0040 | 0.0758 | 0.0529 | 18.8919 |
| Skin | 0.0257 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0138 | 0.0275 | 0.5011 | 1.9955 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0145 | 0.0102 | 1.4225 | 0.7030 |
| Stomach-esophagus | 0.0000 | 0.0077 | 0.0000 | undef |
| Muscle-skeleton | 0.0206 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0190 | 0.0137 | 1.3878 | 0.7206 |
| Pancreas | 0.0050 | 0.0110 | 0.4487 | 2.2286 |
| Penis | 0.0180 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0087 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0203 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0152 | 0.0136 | 1.1223 | 0.8911 |
| Uterus-general | 0.0153 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0096 | | | |
| Prostate hyperplasia | 0.0149 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0353 | | | |
| White blood cells | 0.0043 | | | |
| Cervix | 0.0000 | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | 0.0000 | Breast | 0.0204 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.1595 |
| Brain | 0.0000 | Ovary_t | 0.0253 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0192 |
| Hepatic | 0.0260 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0057 |
| Lung | 0.0000 | Skin-muscle | 0.0324 |
| Suprarenal gland | 0.0000 | Testicles | 0.0154 |
| Kidney | 0.0185 | Lung | 0.0000 |
| Placenta | 0.1030 | Nerves | 0.0151 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0251 | Sensory Organs | 0.0077 |
| | | Uterus_n | 0.0208 |

Electronic Northern for SEQ. ID NO.: 105

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0115 | 0.0132 | 0.8750 | 1.1429 |
| Small intestine | 0.0092 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0090 | 0.0052 | 1.7269 | 0.5791 |
| Endocrine tissue | 0.0034 | 0.0050 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0115 | 0.0000 | undef | 0.0000 |
| Brain | 0.0030 | 0.0041 | 0.7200 | 1.3890 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0129 | 0.0000 | undef |
| Heart | 0.0127 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0117 | 0.0000 | undef |
| Lung | 0.0042 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0097 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0051 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0027 | 0.0068 | 0.3965 | 2.5219 |
| Pancreas | 0.0050 | 0.0000 | undef | 0.0000 |
| Penis | 0.0180 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0109 | 0.0085 | 1.2795 | 0.7815 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0051 | 0.0000 | undef | u.0000 |
| Breast hyperplasia | 0.0064 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0178 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0319 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED LIBRARIES | |
|---------------------|-------------|--------------------------------------|-------------|
| | % frequency | | % frequency |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0125 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0099 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0107 | Hematopoietic | 0.0000 |
| Lung | 0.0108 | Skin-muscle | 0.0259 |
| Suprarenal gland | 0.0254 | Testicles | 0.0000 |
| Kidney | 0.0000 | | 0.0082 |
| Placenta | 0.0121 | Lung | 0.0100 |
| Prostate | 0.0249 | Nerves | 0.0000 |
| Sensory organs | 0.0000 | Prostate | 0.0000 |
| | | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0042 |

Electronic Northern for SEQ. ID NO.: 106

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|---------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0312 | 0.0077 | 4.0678 | 0.2458 |
| Breast | 0.0192 | 0.0019 | 10.2079 | 0.0980 |
| Small intestine | 0.0061 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0060 | 0.0390 | 0.1535 | 6.5146 |
| Endocrine tissue | 0.0068 | 0.0075 | 0.9057 | 1.1042 |
| Gastrointestinal | 0.0057 | 0.0046 | 1.2425 | 0.8048 |
| Brain | 0.0118 | 0.0164 | 0.7200 | 1.3890 |
| Hematopoietic | 0.0080 | 0.0379 | 0.2117 | 4.7230 |
| Skin | 0.0184 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0129 | 0.0000 | undef |
| Heart | 0.0191 | 0.0275 | 0.6939 | 1.4412 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0239 | 0.0102 | 2.3370 | 0.4279 |
| Stomach-esophagus | 0.0000 | 0.0307 | 0.0000 | undef |
| Muscle-skeleton | 0.0051 | 0.0240 | 0.2142 | 4.6693 |
| Kidney | 0.0081 | 0.0137 | 0.5948 | 1.6813 |
| Pancreas | 0.0033 | 0.0110 | 0.2991 | 3.3428 |
| Penis | 0.0120 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0022 | 0.0021 | 1.0236 | 0.9769 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0204 | 0.0000 | undef |
| Uterus-general | 0.0153 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0320 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0178 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0087 | | | |
| Cervix | 0.0319 | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | % frequency | |
| Development | 0.0278 | Breast | 0.0000 |
| Gastrointestinal | 0.0167 | Ovary_n | 0.0000 |
| Brain | 0.0125 | Ovary_t | 0.0203 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0245 |
| Skin | 0.0000 | Fetal | 0.0198 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0213 | Hematopoietic | 0.0171 |
| Lung | 0.0191 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0507 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0082 |
| Placenta | 0.0121 | Nerves | 0.0161 |
| Prostate | 0.0000 | Prostate | 0.0137 |
| Sensory organs | 0.2762 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0208 |

Electronic Northern for SEQ. ID NO.: 107

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0013 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0063 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 108

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|---------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0195 | 0.0000 | undef | 0.0000 |
| Breast | 0.0038 | 0.0036 | 0.6905 | 1.4694 |
| Small intestine | 0.0061 | 0.0165 | 0.3707 | 2.6973 |
| Ovary | 0.0030 | 0.0052 | 0.5756 | 1.7372 |
| Endocrine tissue | 0.0017 | 0.0100 | 0.1698 | 5.8889 |
| Gastrointestinal | 0.0096 | 0.0000 | undef | 0.0000 |
| Brain | 0.0022 | 0.0103 | 0.2160 | 4.6299 |
| Hematopoietic | 0.0027 | 0.0758 | 0.0353 | 28.3379 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0042 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0125 | 0.0061 | 2.0321 | 0.4921 |
| Stomach-esophagus | 0.0097 | 0.0000 | undef | 0.0000 |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0000 | 0.0137 | 0.0000 | undef |
| Pancreas | 0.0000 | 0.0221 | 0.0000 | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0065 | 0.0021 | 3.0709 | 0.3256 |
| Uterus-endometrium | 0.0000 | 0.0528 | 0.0000 | undef |
| Uterus-myometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0095 | | | |
| Cervix | 0.0000 | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | | LIBRARIES | |
| | % frequency | % frequency | |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0759 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0057 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0164 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0274 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0083 |

Electronic Northern for SEQ. ID NO.: 109

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0507 | 0.0179 | 2.8330 | 0.3530 |
| Breast | 0.0153 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0276 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0270 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0119 | 0.0075 | 1.5849 | 0.6309 |
| Gastrointestinal | 0.0096 | 0.0046 | 2.0708 | 0.4829 |
| Brain | 0.0044 | 0.0010 | 4.3198 | 0.2315 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0201 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0115 | 0.0000 | undef | 0.0000 |
| Lung | 0.0073 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0580 | 0.0230 | 2.5211 | 0.3967 |
| Muscle-skeleton | 0.0771 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0000 | 0.0068 | 0.0000 | undef |
| Pancreas | 0.0033 | 0.0221 | 0.1496 | 6.6857 |
| Penis | 0.0210 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0174 | 0.0106 | 1.6378 | 0.6106 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0229 | 0.0068 | 3.3668 | 0.2970 |
| Uterus-general | 0.0357 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0096 | | | |
| Prostate hyperplasia | 0.0149 | | | |
| Seminal vesicle | 0.0514 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0000 | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | 0.0000 | Breast | 0.0816 |
| Gastrointestinal | 0.0083 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0041 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0244 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0097 |
| Suprarenal gland | 0.0507 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0000 |
| Placenta | 0.0242 | Nerves | 0.0030 |
| Prostate | 0.0748 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0042 |

Electronic Northern for SEQ. ID NO.: 110

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0230 | 0.0038 | 6.1248 | 0.1633 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0120 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0136 | 0.0025 | 5.4340 | 0.1840 |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0022 | 0.0031 | 0.7200 | 1.3990 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0184 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0212 | 0.0137 | 1.5420 | 0.6485 |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0156 | 0.0164 | 0.9526 | 1.0498 |
| Lung | 0.0000 | 0.0077 | 0.0000 | undef |
| Stomach-esophagus | 0.0069 | 0.0180 | 0.3807 | 2.6265 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0017 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0060 | 0.0000 | undef | 0.0000 |
| Penis | 0.0000 | 0.0043 | 0.0000 | undef |
| Prostate | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0305 | 0.0068 | 4.4891 | 0.2228 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0192 | | | |
| Breast hyperplasia | 0.0089 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0235 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0532 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0417 | Breast | 0.0204 |
| Gastrointestinal | 0.0056 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0064 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0213 | Hematopoietic | 0.0000 |
| Lung | 0.0072 | Skin-muscle | 0.0162 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0124 | Lung | 0.0000 |
| Placenta | 0.0121 | Nerves | 0.0080 |
| Prostate | 0.0249 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0125 |

Electronic Northern for SEQ. ID NO.: 111

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|---------|---------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0312 | 0.0026 | 12.2035 | 0.0819 |
| Breast | 0.0051 | 0.0019 | 2.7221 | 0.3674 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0025 | 0.0000 | undef |
| Endocrine tissue | 0.0017 | 0.0025 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0038 | 0.0000 | undef | 0.0000 |
| Brain | 0.0022 | 0.0041 | 0.5400 | 1.8520 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0011 | 0.0137 | 0.0771 | 12.9706 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0021 | 0.0020 | 1.0161 | 0.9842 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0034 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0081 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0017 | 0.0055 | 0.2991 | 3.3428 |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0044 | 0.0021 | 2.0473 | 0.4885 |
| Uterus-endometrium | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0051 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0000 | 0.0032 | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0009 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | % frequency | |
| Development | 0.0000 | Breast | 0.0340 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0065 |
| Suprarenal gland | 0.0254 | Testicles | 0.0000 |
| Kidney | 0.0124 | Lung | 0.0082 |
| Placenta | 0.0121 | Nerves | 0.0020 |
| Prostate | 0.0000 | Nerves | 0.0205 |
| Sensory organs | 0.0000 | Prostate | 0.0000 |
| | | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 112

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0013 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0000 | 0.0021 | 0.0000 | undef |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0021 | 0.0137 | 0.1542 | 6.4853 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0010 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0027 | 0.0068 | 0.3965 | 2.5219 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0021 | 0.0000 | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myoetrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0032 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0118 | | | |
| Sensory organs | 0.0043 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0023 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0017 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0114 |
| Lung | 0.0000 | Skin-muscle | 0.0065 |
| Suprarenal gland | 0.0000 | Testicles | 0.0154 |
| Kidney | 0.0000 | Lung | 3.0092 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 113

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|---------|---------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0312 | 0.0026 | 12.2035 | 0.0819 |
| Breast | 0.0102 | 0.0019 | 5.4442 | 0.1837 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0060 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0000 | 0.0050 | 0.0000 | undef |
| Gastrointestinal | 0.0019 | 0.0000 | undef | 0.0000 |
| Brain | 0.0037 | 0.0031 | 1.1999 | 0.8334 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0021 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0042 | 0.0020 | 2.0321 | 0.4921 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0017 | 0.0180 | 0.0952 | 10.5060 |
| Kidney | 0.0054 | 0.0068 | 0.7930 | 1.2610 |
| Pancreas | 0.0017 | 0.0055 | 0.2991 | 3.3428 |
| Penis | 0.0030 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0102 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0032 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0706 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0000 | Breast | 0.0136 |
| Gastrointestinal | 0.0167 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0203 |
| Hematopoietic | 0.0039 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0140 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0000 |
| Placenta | 0.0667 | Nerves | 0.0000 |
| Prostate | 0.0249 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 114

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0039 | 0.0000 | undef |
| Small intestine | 0.0092 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0030 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0007 | 0.0031 | 0.2400 | 4.1669 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0021 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0021 | 0.0020 | 1.0161 | 0.9842 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0068 | 0.0000 | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0022 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0069 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0017 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | 0.0000 | Breast | 0.0068 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0005 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 115

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0195 | 0.0026 | 7.6272 | 0.1311 |
| Breast | 0.0038 | 0.0019 | 2.0416 | 0.4898 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0120 | 0.0052 | 2.3025 | 0.4343 |
| Endocrine tissue | 0.0068 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0038 | 0.0000 | undef | 0.0000 |
| Brain | 0.0007 | 0.0051 | 0.1440 | 6.9448 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0129 | 0.0000 | undef |
| Heart | 0.0042 | 0.0137 | 0.3084 | 3.2426 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0034 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0066 | 0.0276 | 0.2393 | 4.1785 |
| Penis | 0.0000 | 0.0267 | 0.0000 | undef |
| Prostate | 0.0022 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0089 | | | |
| Prostate hyperplasia | 0.0178 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0035 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0017 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0057 |
| Lung | 0.0036 | Skin-muscle | 0.0130 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0062 | Lung | 0.0020 |
| Placenta | 0.0121 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0083 |
| | | Uterus_n | |

Electronic Northern for SEQ. ID NO.: 116

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0624 | 0.0204 | 3.0509 | 0.3278 |
| Breast | 0.0102 | 0.0000 | undef | 0.0000 |
| Small intestine | 0.0368 | 0.0165 | 2.2244 | 0.4496 |
| Ovary | 0.0120 | 0.0026 | 4.6050 | 0.2172 |
| Endocrine tissue | 0.0000 | 0.0050 | 0.0000 | undef |
| Gastrointestinal | 0.0556 | 0.0000 | undef | 0.0000 |
| Brain | 0.0030 | 0.0041 | 0.7200 | 1.3890 |
| Hematopoietic | 0.0053 | 0.0000 | undef | 0.0000 |
| Skin | 0.0110 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0190 | 0.0065 | 2.9412 | 0.3400 |
| Heart | 0.0042 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0031 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0290 | 0.0230 | 1.2605 | 0.7933 |
| Muscle-skeleton | 0.0103 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0033 | 0.0110 | 0.2991 | 3.3428 |
| Penis | 0.1258 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0479 | 0.0319 | 1.5013 | 0.6661 |
| Uterus-endometrium | 0.0338 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.1067 | 0.0272 | 3.9279 | 0.2546 |
| Uterus-general | 0.0509 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0128 | | | |
| Prostate hyperplasia | 0.0476 | | | |
| Seminal vesicle | 0.0267 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0213 | | | |

FETUS
% frequencySTANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0167 |
| Brain | 0.0000 |
| Hematopoietic | 0.0118 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0071 |
| Lung | 0.0000 |
| Suprarenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0000 |
| Prostate | 0.0499 |
| Sensory organs | 0.0000 |

| | |
|------------------|--------|
| Breast | 0.0204 |
| Ovary_n | 0.1595 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0082 |
| Gastrointestinal | 0.0610 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0032 |
| Testicles | 0.0000 |
| Lung | 0.0000 |
| Nerves | 0.0060 |
| Prostate | 0.0342 |
| Sensory Organs | 0.0000 |
| Uterus_n | 0.0541 |

Electronic Northern for SEQ. ID NO.: 117

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0000 | 0.0019 | 0.0000 | undef |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef | undef |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0007 | 0.0000 | undef | 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0000 | 0.0000 | undef | undef |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0000 | undef | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0000 | 0.0000 | undef | undef |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | | | |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0235 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

FETUS
% frequency

STANDARDIZED/SUBTRACTED
LIBRARIES
% frequency

| | | | |
|---------------------|--------|------------------|--------|
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0000 |
| Lung | 0.0072 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 118

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0026 | 0.0038 | 0.6805 | 1.4694 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0030 | 0.0026 | 1.1513 | 0.8686 |
| Endocrine tissue | 0.0068 | 0.0150 | 0.4528 | 2.2083 |
| Gastrointestinal | 0.0000 | 0.0000 | undef | undef |
| Brain | 0.0007 | 0.0051 | 0.1440 | 6.9449 |
| Hematopoietic | 0.0027 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0065 | 0.0000 | undef |
| Heart | 0.0064 | 0.0137 | 0.4626 | 2.1618 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0010 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0017 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0110 | 0.0000 | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0044 | 0.0064 | 0.6824 | 1.4654 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0152 | 0.0068 | 2.2445 | 0.4455 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0089 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0026 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0000 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.1595 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0006 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic | 0.0114 |
| Lung | 0.0000 | Skin-muscle | 0.0063 |
| Suprarenal gland | 0.0000 | Testicles | 0.0154 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0061 | Nerves | 0.0020 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0077 |
| | | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 119

| | NORMAL | TUMOR | Ratios | T/N |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | |
| Bladder | 0.0819 | 0.0383 | 2.1356 | 0.4682 |
| Breast | 0.0473 | 0.0320 | 1.4811 | 0.6752 |
| Small intestine | 0.0460 | 0.0331 | 1.3903 | 0.7193 |
| Ovary | 0.0539 | 0.0442 | 1.2190 | 0.8204 |
| Endocrine tissue | 0.0494 | 0.0652 | 0.7576 | 1.3199 |
| Gastrointestinal | 0.0805 | 0.0139 | 5.7984 | 0.1725 |
| Brain | 0.0451 | 0.0390 | 1.1557 | 0.8653 |
| Hematopoietic | 0.0374 | 0.0379 | 0.9881 | 1.0121 |
| Skin | 0.0367 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0190 | 0.0323 | 0.5882 | 1.7000 |
| Heart | 0.0382 | 0.0825 | 0.4626 | 2.1618 |
| Testicles | 0.0173 | 0.0117 | 1.4759 | 0.6775 |
| Lung | 0.0384 | 0.0184 | 2.0886 | 0.4788 |
| Stomach-esophagus | 0.0580 | 0.0537 | 1.0805 | 0.9255 |
| Muscle-skeleton | 0.0514 | 0.0240 | 2.1416 | 0.4669 |
| Kidney | 0.0489 | 0.0479 | 1.0196 | 0.9808 |
| Pancreas | 0.0330 | 0.0663 | 0.4986 | 2.0057 |
| Penis | 0.0359 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0610 | 0.0617 | 0.9883 | 1.0118 |
| Uterus-endometrium | 0.2838 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0305 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0509 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.2206 | | | |
| Prostate hyperplasia | 0.0773 | | | |
| Seminal vesicle | 0.0089 | | | |
| Sensory organs | 0.0353 | | | |
| White blood cells | 0.0737 | | | |
| Cervix | 0.0319 | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | 0.0278 | Breast | 0.0340 |
| Gastrointestinal | 0.0361 | Ovary_n | 0.1595 |
| Brain | 0.0125 | Ovary_t | 0.0101 |
| Hematopoietic | 0.0157 | Endocrine tissue | 0.0490 |
| Skin | 0.0000 | Fetal | 0.0233 |
| Hepatic | 0.0260 | Gastrointestinal | 0.0488 |
| Heart-blood vessels | 0.0818 | Hematopoietic | 0.0285 |
| Lung | 0.0325 | Skin-muscle | 0.0227 |
| Suprarenal gland | 0.0000 | Testicles | 0.0154 |
| Kidney | 0.0432 | Lung | 0.0164 |
| Placenta | 0.0303 | Nerves | 0.0261 |
| Prostate | 0.0000 | Prostate | 0.1163 |
| Sensory organs | 0.0126 | Sensory Organs | 0.0929 |
| | | Uterus_n | 0.0416 |

Electronic Northern for SEQ. ID NO.: 120

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0195 | 0.0000 | undef | 0.0000 |
| Breast | 0.0026 | 0.0038 | 0.6805 | 1.4694 |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0017 | 0.0025 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0038 | 0.0000 | undef | 0.0000 |
| Brain | 0.0052 | 0.0041 | 1.2599 | 0.7937 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0011 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0000 | 0.0020 | 0.0000 | undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0034 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0000 | undef | undef |
| Penis | 0.0000 | 0.0000 | undef | undef |
| Prostate | 0.0022 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0026 | | | |
| White blood cells | 0.0106 | | | |
| Cervix | | | | |

| FETUS | STANDARDIZED/SUBTRACTED | |
|-------------|-------------------------|--------|
| % frequency | LIBRARIES | |
| | % frequency | |
| 0.0000 | Breast | 0.0000 |
| 0.0000 | Ovary_n | 0.0000 |
| 0.0000 | Ovary_t | 0.0000 |
| 0.0000 | Endocrine tissue | 0.0000 |
| 0.0000 | Fetal | 0.0006 |
| 0.0000 | Gastrointestinal | 0.0000 |
| 0.0000 | Hematopoietic | 0.0000 |
| 0.0000 | Skin-muscle | 0.0000 |
| 0.0254 | Testicles | 0.0000 |
| 0.0062 | Lung | 0.0070 |
| 0.0000 | Nerves | 0.0000 |
| 0.0000 | Prostate | 0.0000 |
| 0.0000 | Sensory Organs | 0.0000 |
| | Uterus_n | 0.0000 |

Electronic Northern for SEQ. ID NO.: 121

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0273 | 0.0051 | 5.3391 | 0.1873 |
| Breast | 0.0000 | 0.0000 | undef | undef |
| Small intestine | 0.0031 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0030 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0000 | 0.0025 | 0.0000 | undef |
| Gastrointestinal | 0.0038 | 0.0000 | undef | 0.0000 |
| Brain | 0.0059 | 0.0041 | 1.4399 | 0.6945 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0000 | 0.0000 | undef | undef |
| Hepatic | 0.0048 | 0.0000 | undef | 0.0000 |
| Heart | 0.0032 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0117 | 0.0000 | undef |
| Lung | 0.0052 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0000 | 0.0077 | 0.0000 | undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef | undef |
| Kidney | 0.0000 | 0.0000 | undef | undef |
| Pancreas | 0.0017 | 0.0000 | undef | 0.0000 |
| Penis | 0.0150 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0109 | 0.0085 | 1.2795 | 0.7815 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0076 | 0.0000 | undef | 0.0000 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0000 | | | |
| Prostate hyperplasia | 0.0089 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| % frequency | | LIBRARIES | |
| | % frequency | | |
| Development | 0.0000 | Breast | 0.0136 |
| Gastrointestinal | 0.0028 | Ovary_n | 0.1595 |
| Brain | 0.0000 | Ovary_t | 0.0051 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0245 |
| Skin | 0.0000 | Fetal | 0.0035 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0000 | Testicles | 0.0077 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0000 | Nerves | 0.0030 |
| Prostate | 0.0000 | Prostate | 0.0068 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0167 |

Electronic Northern for SEQ. ID NO.: 122

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0351 | 0.0077 | 4.5763 | 0.2185 |
| Breast | 0.0077 | 0.0038 | 2.0416 | 0.4899 |
| Small intestine | 0.0184 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0000 | 0.0000 | undef | undef |
| Endocrine tissue | 0.0017 | 0.0000 | undef | 0.0000 |
| Gastrointestinal | 0.0115 | 0.0093 | 1.2425 | 0.8048 |
| Brain | 0.0030 | 0.0021 | 1.4399 | 0.6945 |
| Hematopoietic | 0.0013 | 0.0000 | undef | 0.0000 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0095 | 0.0000 | undef | 0.0000 |
| Heart | 0.0233 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0021 | 0.0000 | undef | 0.0000 |
| Stomach-esophagus | 0.0000 | 0.0077 | 0.0000 | undef |
| Muscle-skeleton | 0.0103 | 0.0000 | undef | 0.0000 |
| Kidney | 0.0054 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0035 | 0.0000 | undef |
| Penis | 0.0599 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0131 | 0.0149 | 0.8774 | 1.1397 |
| Uterus-endometrium | 0.0068 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0152 | 0.0340 | 0.4489 | 2.2276 |
| Uterus-general | 0.0407 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0064 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0178 | | | |
| Sensory organs | 0.0118 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | 0.0000 | | | |

| FETUS | | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0278 | Breast | 0.0136 |
| Gastrointestinal | 0.0139 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0152 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0052 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0391 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0032 |
| Suprarenal gland | 0.0254 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0000 |
| Placenta | 0.0061 | Nerves | 0.0060 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0077 |
| | | Uterus_n | 0.0083 |

Electronic Northern for SEQ. ID NO.: 123

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0390 | 0.0051 | 7.6272 | 0.1311 |
| Breast | 0.0064 | 0.0056 | 1.1342 | 0.8817 |
| Small intestine | 0.0184 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0060 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0017 | 0.0050 | 0.3396 | 2.9444 |
| Gastrointestinal | 0.0057 | 0.0000 | undef | 0.0000 |
| Brain | 0.0007 | 0.0021 | 0.3600 | 2.7779 |
| Hematopoietic | 0.0040 | 0.0000 | undef | 0.0000 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0095 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef | undef |
| Lung | 0.0021 | 0.0020 | 1.0161 | 0.9842 |
| Stomach-esophagus | 0.0193 | 0.0077 | 2.5211 | 0.3967 |
| Muscle-skeleton | 0.0154 | 0.0060 | 2.5700 | 0.3891 |
| Kidney | 0.0054 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0000 | 0.0055 | 0.0000 | undef |
| Penis | 0.0210 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0044 | 0.0000 | undef | 0.0000 |
| Uterus-endometrium | 0.0203 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0152 | 0.0272 | 0.5611 | 1.7821 |
| Uterus-general | 0.0000 | 0.0000 | undef | undef |
| Breast hyperplasia | 0.0128 | | | |
| Prostate hyperplasia | 0.0059 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0017 | | | |
| White blood cells | 0.0000 | | | |
| Cervix | | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0083 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0012 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0142 | Hematopoietic | 0.0000 |
| Lung | 0.0000 | Skin-muscle | 0.0065 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0082 |
| Placenta | 0.0000 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0000 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0083 |

Electronic Northern for SEQ. ID NO.: 125

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0390 | 0.0051 | 7.6272 | 0.1311 |
| Breast | 0.0153 | 0.0150 | 1.0208 | 0.9796 |
| Small intestine | 0.0245 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0210 | 0.0078 | 2.6863 | 0.3723 |
| Endocrine tissue | 0.0170 | 0.0125 | 1.3585 | 0.7361 |
| Gastrointestinal | 0.0153 | 0.0000 | undef | 0.0000 |
| Brain | 0.0126 | 0.0133 | 0.9415 | 1.0622 |
| Hematopoietic | 0.0067 | 0.0000 | undef | 0.0000 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0129 | 0.0000 | undef |
| Heart | 0.0127 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0115 | 0.0117 | 0.9839 | 1.0163 |
| Lung | 0.0114 | 0.0143 | 0.7983 | 1.2326 |
| Stomach-esophagus | 0.0097 | 0.0307 | 0.3151 | 3.1733 |
| Muscle-skeleton | 0.0034 | 0.0060 | 0.5711 | 1.7510 |
| Kidney | 0.0326 | 0.0274 | 1.1896 | 0.8406 |
| Pancreas | 0.0033 | 0.0166 | 0.1994 | 5.0142 |
| Penis | 0.0629 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0109 | 0.0170 | 0.6398 | 1.5631 |
| Uterus-endometrium | 0.0203 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0305 | 0.0068 | 4.4891 | 0.2228 |
| Uterus-general | 0.0255 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0256 | | | |
| Prostate hyperplasia | 0.0208 | | | |
| Seminal vesicle | 0.0178 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0191 | | | |
| Cervix | 0.0106 | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | % frequency | |
| Development | 0.0000 | Breast | |
| Gastrointestinal | 0.0111 | Ovary_n | 0.0000 |
| Brain | 0.0063 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0000 | Endocrine tissue | 0.0051 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0076 |
| Heart-blood vessels | 0.0036 | Hematopoietic | 0.0000 |
| Lung | 0.0072 | Skin-muscle | 0.0057 |
| Suprarenal gland | 0.0254 | Testicles | 0.0162 |
| Kidney | 0.0062 | Lung | 0.0077 |
| Placenta | 0.0000 | Nerves | 0.0082 |
| Prostate | 0.0000 | Nerves | 0.0120 |
| Sensory organs | 0.0126 | Prostate | 0.0205 |
| | | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0749 |

Electronic Northern for SEQ. ID NO.: 126

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|---------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0051 | 0.0056 | 0.9074 | 1.1021 |
| Small intestine | 0.0184 | 0.0000 | undef | 0.0000 |
| Ovary | 0.0060 | 0.0104 | 0.5756 | 1.7372 |
| Endocrine tissue | 0.0085 | 0.0075 | 1.1321 | 0.8833 |
| Gastrointestinal | 0.0096 | 0.0000 | undef | 0.0000 |
| Brain | 0.0059 | 0.0154 | 0.3840 | 2.6043 |
| Hematopoietic | 0.0080 | 0.0000 | undef | 0.0000 |
| Skin | 0.0073 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0095 | 0.0129 | 0.7353 | 1.3600 |
| Heart | 0.0201 | 0.0137 | 1.4649 | 0.6827 |
| Testicles | 0.0058 | 0.0000 | undef | 0.0000 |
| Lung | 0.0145 | 0.0164 | 0.8891 | 1.1248 |
| Stomach-esophagus | 0.0000 | 0.0230 | 0.0000 | undef |
| Muscle-skeleton | 0.0017 | 0.0300 | 0.0571 | 17.5100 |
| Kidney | 0.0217 | 0.0068 | 3.1722 | 0.3152 |
| Pancreas | 0.0050 | 0.0000 | undef | 0.0000 |
| Penis | 0.0210 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0065 | 0.0021 | 3.0709 | 0.3256 |
| Uterus-endometrium | 0.0135 | 0.0000 | undef | 0.0000 |
| Uterus-myometrium | 0.0457 | 0.0204 | 2.2445 | 0.4455 |
| Uterus-general | 0.0153 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0096 | | | |
| Prostate hyperplasia | 0.0000 | | | |
| Seminal vesicle | 0.0000 | | | |
| Sensory organs | 0.0470 | | | |
| White blood cells | 0.0121 | | | |
| Cervix | 0.0213 | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|--------|
| | % frequency | LIBRARIES | |
| | | % frequency | |
| Development | 0.0139 | Breast | |
| Gastrointestinal | 0.0056 | Ovary_n | 0.0068 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0157 | Endocrine tissue | 0.0101 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0210 |
| Heart-blood vessels | 0.0213 | Hematopoietic | 0.0122 |
| Lung | 0.0217 | Skin-muscle | 0.0057 |
| Suprarenal gland | 0.0254 | Testicles | 0.0259 |
| Kidney | 0.0185 | Lung | 0.0000 |
| Placenta | 0.0121 | Nerves | 0.0000 |
| Prostate | 0.0000 | Prostate | 0.0020 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0387 |
| | | | 0.0000 |

Electronic Northern for SEQ. ID NO.: 127

| | NORMAL | TUMOR | Ratios | |
|----------------------|-------------|-------------|--------|--------|
| | % frequency | % frequency | N/T | T/N |
| Bladder | 0.0156 | 0.0000 | undef | 0.0000 |
| Breast | 0.0090 | 0.0019 | 4.7637 | 0.2099 |
| Small intestine | 0.0000 | 0.0000 | undef | undef |
| Ovary | 0.0240 | 0.0000 | undef | 0.0000 |
| Endocrine tissue | 0.0017 | 0.0025 | 0.6792 | 1.4722 |
| Gastrointestinal | 0.0000 | 0.0046 | 0.0000 | undef |
| Brain | 0.0037 | 0.0010 | 3.5998 | 0.2779 |
| Hematopoietic | 0.0000 | 0.0000 | undef | undef |
| Skin | 0.0037 | 0.0000 | undef | 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef | undef |
| Heart | 0.0074 | 0.0000 | undef | 0.0000 |
| Testicles | 0.0058 | 0.0234 | 0.2460 | 4.0652 |
| Lung | 0.0010 | 0.0061 | 0.1693 | 5.9051 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef | undef |
| Muscle-skeleton | 0.0000 | 0.0060 | 0.0000 | undef |
| Kidney | 0.0027 | 0.0000 | undef | 0.0000 |
| Pancreas | 0.0017 | 0.0110 | 0.1496 | 6.6857 |
| Penis | 0.0090 | 0.0000 | undef | 0.0000 |
| Prostate | 0.0044 | 0.0064 | 0.6824 | 1.4654 |
| Uterus-endometrium | 0.0000 | 0.0000 | undef | undef |
| Uterus-myometrium | 0.0223 | 0.0136 | 1.6834 | 0.5940 |
| Uterus-general | 0.0102 | 0.0000 | undef | 0.0000 |
| Breast hyperplasia | 0.0032 | | | |
| Prostate hyperplasia | 0.0119 | | | |
| Seminal vesicle | 0.0267 | | | |
| Sensory organs | 0.0000 | | | |
| White blood cells | 0.0017 | | | |
| Cervix | 0.0000 | | | |

| | FETUS | STANDARDIZED/SUBTRACTED | |
|---------------------|-------------|-------------------------|-------------|
| | % frequency | LIBRARIES | % frequency |
| Development | 0.0139 | Breast | 0.0000 |
| Gastrointestinal | 0.0000 | Ovary_n | 0.0000 |
| Brain | 0.0000 | Ovary_t | 0.0000 |
| Hematopoietic | 0.0079 | Endocrine tissue | 0.0000 |
| Skin | 0.0000 | Fetal | 0.0000 |
| Hepatic | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0071 | Hematopoietic | 0.0000 |
| Lung | 0.0036 | Skin-muscle | 0.0000 |
| Suprarenal gland | 0.0000 | Testicles | 0.0000 |
| Kidney | 0.0000 | Lung | 0.0092 |
| Placenta | 0.0000 | Nerves | 0.0010 |
| Prostate | 0.0000 | Prostate | 0.0205 |
| Sensory organs | 0.0000 | Sensory Organs | 0.0000 |
| | | Uterus_n | 0.0042 |

Electronic Northern for Seq. ID: 391

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | 0.0025 | 0.0000 | undef 0.0000 |
| Bladder | 0.0312 | 0.0000 | undef 0.0000 |
| Breast | 0.0079 | 0.0056 | 1.4090 0.7097 |
| Large intestine | 0.0077 | 0.0000 | undef 0.0000 |
| Small intestine | 0.0027 | 0.0107 | 0.2577 1.8812 |
| Ovary | 0.0030 | 0.0072 | 0.4148 2.4109 |
| Endocrine tissue | 0.0048 | 0.0089 | 0.5432 1.8409 |
| Brain | 0.0029 | 0.0080 | 0.3627 2.7574 |
| Skin | 0.0000 | 0.0000 | undef undef |
| Hepatic | 0.0093 | 0.0000 | undef 0.0000 |
| Heart | 0.0020 | 0.0000 | undef 0.0000 |
| Testicles | 0.0000 | 0.0118 | 0.0000 undef |
| Lung | 0.0010 | 0.0037 | 0.2631 1.8007 |
| Stomach-esophagus | 0.0217 | 0.0000 | undef 0.0000 |
| Muscle-skeleton | 0.0034 | 0.0000 | undef 0.0000 |
| Kidney | 0.0045 | 0.0048 | 0.9285 1.0770 |
| Pancreas | 0.0017 | 0.0055 | 0.2992 3.3427 |
| Prostate | 0.0066 | 0.0039 | 1.6882 0.5923 |
| T lymphoma | 0.0025 | 0.0149 | 0.1691 5.9152 |
| Uterus | 0.0030 | 0.0046 | 0.6426 1.5563 |
| White blood cells | 0.0021 | 0.0000 | undef 0.0000 |
| Hematopoietic | 0.0000 | | |
| Penis | 0.0134 | | |
| Seminal vesicle | 0.0070 | | |
| Sensory organs | 0.0000 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0278 |
| Gastrointestinal | 0.0000 |
| Brain | 0.0188 |
| Hematopoietic | 0.0079 |
| Skin | 0.0000 |
| Hepatic | 0.0260 |
| Heart-blood vessels | 0.0071 |
| Lung | 0.0000 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0126 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0000 |
| Breast_t | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0245 |
| Gastrointestinal | 0.0064 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0065 |
| Testicles_t | 0.0157 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0000 |
| Nerves | 0.0000 |
| Kidney_t | 0.0060 |
| Ovary uterus | 0.0000 |
| Prostate_n | 0.0090 |
| Sensory organs | 0.0132 |
| White blood cells | 0.0000 |
| | 0.0000 |

Electronic Northern for Seq. ID: 392

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | 0.0000 | 0.0000 | undef undef |
| Bladder | 0.0156 | 0.0000 | undef 0.0000 |
| Breast | 0.0000 | 0.0000 | undef undef |
| Large intestine | 0.0000 | 0.0000 | undef undef |
| Small intestine | 0.0000 | 0.0000 | undef undef |
| Ovary | 0.0059 | 0.0000 | undef 0.0000 |
| Endocrine tissue | 0.0000 | 0.0000 | undef undef |
| Brain | 0.0000 | 0.0000 | undef undef |
| Skin | 0.0000 | 0.0000 | undef undef |
| Hepatic | 0.0000 | 0.0000 | undef undef |
| Heart | 0.0000 | 0.0000 | undef undef |
| Testicles | 0.0010 | 0.0000 | undef 0.0000 |
| Lung | 0.0000 | 0.0000 | undef undef |
| Stomach-esophagus | 0.0000 | 0.0000 | undef undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef undef |
| Kidney | 0.0000 | 0.0000 | undef undef |
| Pancreas | 0.0000 | 0.0000 | undef undef |
| Prostate | 0.0000 | 0.0000 | undef undef |
| T lymphoma | 0.0000 | 0.0000 | undef undef |
| Uterus | 0.0000 | 0.0000 | undef undef |
| White blood cells | 0.0000 | 0.0000 | undef undef |
| Hematopoietic | 0.0000 | | |
| Penis | 0.0000 | | |
| Seminal vesicle | 0.0000 | | |
| Sensory organs | 0.0000 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0000 |
| Brain | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung | 0.0000 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0000 |
| Breast_t | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0000 |
| Gastrointestinal | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0000 |
| Nerves | 0.0010 |
| Kidney_t | 0.0000 |
| Ovary uterus | 0.0023 |
| Prostate_n | 0.0000 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |

Electronic Northern for Seq. ID: 393

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | 0.0075 | 0.0000 | undef 0.0000 |
| Bladder | 0.0195 | 0.0000 | undef 0.0000 |
| Breast | 0.0009 | 0.0000 | undef 0.0000 |
| Large intestine | 0.0037 | 0.0000 | undef 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef undef |
| Ovary | 0.0000 | 0.0000 | undef undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef undef |
| Brain | 0.0000 | 0.0000 | undef undef |
| Skin | 0.0000 | 0.0000 | undef undef |
| Hepatic | 0.0000 | 0.0000 | undef undef |
| Heart | 0.0046 | 0.0000 | undef 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef undef |
| Lung | 0.0000 | 0.0000 | undef undef |
| Stomach-esophagus | 0.0010 | 0.0000 | undef 0.0000 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef undef |
| Kidney | 0.0034 | 0.0000 | undef 0.0000 |
| Pancreas | 0.0000 | 0.0000 | undef undef |
| Prostate | 0.0000 | 0.0055 | 0.0000 undef |
| T lymphoma | 0.0000 | 0.0000 | undef undef |
| Uterus | 0.0000 | 0.0000 | undef undef |
| White blood cells | 0.0000 | 0.0000 | undef undef |
| Hematopoietic | 0.0000 | 0.0000 | undef undef |
| Penis | 0.0027 | | |
| Seminal vesicle | 0.0000 | | |
| Sensory organs | 0.0000 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0000 |
| Brain | 0.0063 |
| Hematopoietic | 0.0039 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung | 0.0000 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0061 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0000 |
| Breast_t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0029 |
| Gastrointestinal | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0042 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0000 |
| Nerves | 0.0020 |
| Kidney_t | 0.0000 |
| Ovary Uterus | 0.0045 |
| Prostate_n | 0.0000 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |

Electronic Northern for Seq. ID: 394

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | 0.0000 | 0.0136 | 0.0000 undef |
| Bladder | 0.0156 | 0.0023 | 6.6380 0.1506 |
| Breast | 0.0035 | 0.0042 | 0.8349 1.1977 |
| Large intestine | 0.0038 | 0.0199 | 0.1922 5.2023 |
| Small intestine | 0.0000 | 0.0000 | undef undef |
| Ovary | 0.0059 | 0.0024 | 2.4887 0.4018 |
| Endocrine tissue | 0.0080 | 0.0000 | undef 0.0000 |
| Brain | 0.0023 | 0.0040 | 0.5803 1.7234 |
| Skin | 0.0073 | 0.0000 | undef 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef undef |
| Heart | 0.0030 | 0.0000 | undef 0.0000 |
| Testicles | 0.0000 | 0.0059 | 0.0000 undef |
| Lung | 0.0013 | 0.0053 | 0.3508 2.8506 |
| Stomach-esophagus | 0.0072 | 0.0000 | undef 0.0000 |
| Muscle-skeleton | 0.0017 | 0.0000 | undef 0.0000 |
| Kidney | 0.0045 | 0.0048 | 0.9285 1.0770 |
| Pancreas | 0.0033 | 0.0110 | 0.2992 3.3427 |
| Prostate | 0.0057 | 0.0026 | 2.1706 0.4607 |
| T lymphoma | 0.0051 | 0.0149 | 0.3381 2.5576 |
| Uterus | 0.0015 | 0.0000 | undef 0.0000 |
| White blood cells | 0.0021 | 0.0304 | 0.0676 14.7861 |
| Hematopoietic | 0.0013 | | |
| Penis | 0.0054 | | |
| Seminal vesicle | 0.0000 | | |
| Sensory organs | 0.0118 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0028 |
| Brain | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung | 0.0036 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0062 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | |
| Breast_t | 0.0136 |
| Large intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0051 |
| Fetal | 0.0000 |
| Gastrointestinal | 0.0017 |
| Hematopoietic | 0.0122 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0293 |
| Nerves | 0.0000 |
| Kidney_t | 0.0040 |
| Ovary uterus | 0.0000 |
| Prostate_n | 0.0068 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |
| | 0.0000 |

Electronic Northern for Seq. ID: 395

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | 0.0000 | 0.0000 | undef undef |
| Bladder | 0.0156 | 0.0047 | 3.3192 0.3013 |
| Breast | 0.0062 | 0.0183 | 0.3372 2.9657 |
| Large intestine | 0.0019 | 0.0114 | 0.1682 5.9454 |
| Small intestine | 0.0000 | 0.0107 | 0.0000 undef |
| Ovary | 0.0030 | 0.0072 | 0.4148 2.4110 |
| Endocrine tissue | 0.0000 | 0.0000 | undef undef |
| Brain | 0.0006 | 0.0010 | 0.6045 1.6542 |
| Hepatic | 0.0073 | 0.0000 | undef 0.0000 |
| Heart | 0.0000 | 0.0190 | 0.0000 undef |
| Testicles | 0.0020 | 0.0962 | 0.0211 47.4018 |
| Lung | 0.0000 | 0.0000 | undef undef |
| Stomach-esophagus | 0.0039 | 0.0111 | 0.3508 2.8506 |
| Muscle-skeleton | 0.0000 | 0.0000 | undef undef |
| Kidney | 0.0171 | 0.0037 | 4.6389 0.2156 |
| Pancreas | 0.0043 | 0.0000 | undef 0.0000 |
| Prostate | 0.0000 | 0.0110 | 0.0000 undef |
| T lymphoma | 0.0000 | 0.0052 | 0.0000 undef |
| Uterus | 0.0025 | 0.0000 | undef 0.0000 |
| White blood cells | 0.0015 | 0.0000 | undef 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef undef |
| Penis | 0.0013 | | |
| Seminal vesicle | 0.0054 | | |
| Sensory organs | 0.0000 | | |
| | 0.0000 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0278 |
| Gastrointestinal | 0.0056 |
| Brain | 0.0063 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0071 |
| Lung | 0.0000 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0000 |
| Breast_t | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0152 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0006 |
| Gastrointestinal | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0000 |
| Nerves | 0.0000 |
| Kidney_t | 0.0000 |
| Ovary uterus | 0.0113 |
| Prostate_n | 0.0000 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |

Electronic Northern for Seq. ID: 396

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | 0.0000 | 0.0136 | 0.0000 undef |
| Bladder | 0.0429 | 0.0000 | undef 0.0000 |
| Breast | 0.0000 | 0.0042 | 0.0000 undef |
| Large intestine | 0.0038 | 0.0000 | undef 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef undef |
| Ovary | 0.0000 | 0.0000 | undef undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef undef |
| Brain | 0.0032 | 0.0000 | undef 0.0000 |
| Skin | 0.0012 | 0.0010 | 1.1605 0.8617 |
| Hepatic | 0.0037 | 0.0000 | undef 0.0000 |
| Heart | 0.0046 | 0.0000 | undef 0.0000 |
| Testicles | 0.0051 | 0.0000 | undef 0.0000 |
| Lung | 0.0000 | 0.0000 | undef undef |
| Stomach-esophagus | 0.0000 | 0.0055 | 0.0000 undef |
| Muscle-skeleton | 0.0000 | 0.0064 | 0.0000 undef |
| Kidney | 0.0017 | 0.0037 | 0.4639 2.1557 |
| Pancreas | 0.0045 | 0.0000 | undef 0.0000 |
| Prostate | 0.0017 | 0.0000 | undef 0.0000 |
| T lymphoma | 0.0009 | 0.0026 | 0.3618 2.7643 |
| Uterus | 0.0000 | 0.0000 | undef undef |
| White blood cells | 0.0030 | 0.0000 | undef 0.0000 |
| Hematopoietic | 0.0007 | 0.0000 | undef 0.0000 |
| Penis | 0.0000 | | |
| Seminal vesicle | 0.0054 | | |
| Sensory organs | 0.0000 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0000 |
| Brain | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0036 |
| Heart-blood vessels | 0.0000 |
| Lung | 0.0000 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0249 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | |
| Breast_t | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0000 |
| Gastrointestinal | 0.0075 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0084 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0098 |
| Nerves | 0.0000 |
| Kidney_t | 0.0070 |
| Ovary uterus | 0.0000 |
| Prostate_n | 0.0000 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0077 |
| | 0.0000 |

Electronic Northern for Seq. ID: 397

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | 0.0025 | 0.0000 | undef 0.0000 |
| Bladder | 0.0117 | 0.0000 | undef 0.0000 |
| Breast | 0.0009 | 0.0000 | undef 0.0000 |
| Large intestine | 0.0000 | 0.0000 | undef undef |
| Small intestine | 0.0000 | 0.0000 | undef undef |
| Ovary | 0.0030 | 0.0000 | undef 0.0000 |
| Endocrine tissue | 0.0048 | 0.0000 | undef 0.0000 |
| Brain | 0.0006 | 0.0000 | undef 0.0000 |
| Skin | 0.0000 | 0.0000 | undef undef |
| Hepatic | 0.0000 | 0.0063 | 0.0000 undef |
| Heart | 0.0010 | 0.0000 | undef 0.0000 |
| Testicles | 0.0000 | 0.0000 | undef undef |
| Lung | 0.0019 | 0.0018 | 1.0524 0.9502 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef undef |
| Kidney | 0.0000 | 0.0000 | undef undef |
| Pancreas | 0.0000 | 0.0000 | undef undef |
| Prostate | 0.0009 | 0.0026 | 0.3618 2.7643 |
| T lymphoma | 0.0000 | 0.0000 | undef undef |
| Uterus | 0.0000 | 0.0000 | undef undef |
| White blood cells | 0.0007 | 0.0000 | undef 0.0000 |
| Hematopoietic | 0.0000 | | |
| Penis | 0.0000 | | |
| Seminal vesicle | 0.0000 | | |
| Sensory organs | 0.0000 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0028 |
| Brain | 0.0000 |
| Hematopoietic | 0.0039 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung | 0.0000 |
| Adrenal gland | 0.0062 |
| Kidney | 0.0000 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0068 |
| Breast_t | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0051 |
| Fetal | 0.0000 |
| Gastrointestinal | 0.0070 |
| Hematopoietic | 0.0122 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0293 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0000 |
| Nerve_s | 0.0000 |
| Kidney_t | 0.0000 |
| Ovary uterus | 0.0135 |
| Prostate_n | 0.0061 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |

Electronic Northern for Seq. ID: 398

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | 0.0023 | 0.0000 | undef 0.0000 |
| Bladder | 0.0156 | 0.0023 | 6.6384 0.1306 |
| Breast | 0.0033 | 0.0042 | 1.2524 0.7985 |
| Large intestine | 0.0000 | 0.0028 | 0.0000 undef |
| Small intestine | 0.0027 | 0.0000 | undef 0.0000 |
| Ovary | 0.0030 | 0.0024 | 1.2443 0.8037 |
| Endocrine tissue | 0.0000 | 0.0037 | 0.0000 undef |
| Brain | 0.0024 | 0.0060 | 0.4030 2.4814 |
| Skin | 0.0000 | 0.0000 | undef undef |
| Hepatic | 0.0000 | 0.0000 | undef undef |
| Heart | 0.0030 | 0.0137 | 0.2213 4.5145 |
| Testicles | 0.0080 | 0.0000 | undef 0.0000 |
| Lung | 0.0068 | 0.0037 | 1.8417 0.5430 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef undef |
| Muscle-skeleton | 0.0034 | 0.0000 | undef 0.0000 |
| Kidney | 0.0022 | 0.0000 | undef 0.0000 |
| Pancreas | 0.0000 | 0.0055 | 0.0000 undef |
| Prostate | 0.0028 | 0.0026 | 1.0853 0.9214 |
| T lymphoma | 0.0000 | 0.0000 | undef undef |
| Uterus | 0.0000 | 0.0092 | 0.0000 undef |
| White blood cells | 0.0082 | 0.0000 | undef 0.0000 |
| Hematopoietic | 0.0013 | | |
| Penis | 0.0054 | | |
| Seminal vesicle | 0.0070 | | |
| Sensory organs | 0.0000 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0028 |
| Brain | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0036 |
| Heart-blood vessels | 0.0000 |
| Lung | 0.0000 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0068 |
| Breast_t | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0006 |
| Gastrointestinal | 0.0122 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0065 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0000 |
| Nerves | 0.0030 |
| Kidney_t | 3.0000 |
| Ovary uterus | 0.0090 |
| Prostate_n | 0.0000 |
| Sensory organs | 2.0000 |
| White blood cells | 0.0000 |

Electronic Northern for Seq. ID: 399

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | 0.0000 | 0.0136 | 0.0000 undef |
| Bladder | 0.0234 | 0.0047 | 4.9788 0.2009 |
| Breast | 0.0070 | 0.0098 | 0.7157 1.3973 |
| Large intestine | 0.0057 | 0.0085 | 0.6728 1.4864 |
| Small intestine | 0.0110 | 0.0000 | undef 0.0000 |
| Ovary | 0.0059 | 0.0000 | undef 0.0000 |
| Endocrine tissue | 0.0032 | 0.0038 | 0.8479 1.1794 |
| Brain | 0.0018 | 0.0020 | 0.9068 1.1028 |
| Skin | 0.0073 | 0.0000 | undef 0.0000 |
| Hepatic | 0.0046 | 0.0190 | 0.2441 4.0960 |
| Heart | 0.0081 | 0.0000 | undef 0.0000 |
| Testicles | 0.0040 | 0.0000 | undef 0.0000 |
| Lung | 0.0068 | 0.0018 | 3.6834 0.2715 |
| Stomach-esophagus | 0.0072 | 0.0064 | 1.1333 0.8824 |
| Muscle-skeleton | 0.0069 | 0.0000 | undef 0.0000 |
| Kidney | 0.0067 | 0.0096 | 0.6963 1.4362 |
| Pancreas | 0.0033 | 0.0221 | 0.1496 6.6857 |
| Prostate | 0.0094 | 0.0052 | 1.8088 0.5529 |
| T lymphoma | 0.0000 | 0.0000 | undef undef |
| Uterus | 0.0093 | 0.0000 | undef 0.0000 |
| White blood cells | 0.0068 | 0.0000 | undef 0.0000 |
| Hematopoietic | 0.0000 | | |
| Penis | 0.0134 | | |
| Seminal vesicle | 0.0070 | | |
| Sensory organs | 0.0118 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0139 |
| Gastrointestinal | 0.0111 |
| Brain | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung | 0.0145 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0408 |
| Breast_t | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.1595 |
| Endocrine tissue | 0.0101 |
| Fetal | 0.0000 |
| Gastrointestinal | 0.0046 |
| Hematopoietic | 0.0122 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0130 |
| Testicles_t | 0.0125 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0098 |
| Nerves | 0.0000 |
| Kidney_t | 0.0000 |
| Ovary uterus | 0.0000 |
| Prostate_n | 0.0068 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |

Electronic Northern for Seq. ID: 400

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | 0.0000 | 0.0136 | 0.0000 undef |
| Bladder | 0.0156 | 0.0000 | undef 0.0000 |
| Breast | 0.0018 | 0.0000 | undef 0.0000 |
| Large intestine | 0.0000 | 0.0000 | undef undef |
| Small intestine | 0.0000 | 0.0000 | undef undef |
| Ovary | 0.0000 | 0.0000 | undef undef |
| Endocrine tissue | 0.0000 | 0.0000 | undef undef |
| Brain | 0.0015 | 0.0019 | 0.8473 1.1794 |
| Skin | 0.0018 | 0.0010 | 1.8135 0.5514 |
| Hepatic | 0.0073 | 0.0000 | undef 0.0000 |
| Heart | 0.0046 | 0.0000 | undef 0.0000 |
| Testicles | 0.0020 | 0.0000 | undef 0.0000 |
| Lung | 0.0040 | 0.0000 | undef 0.0000 |
| Stomach-esophagus | 0.0000 | 0.0000 | undef undef |
| Muscle-skeleton | 0.0000 | 0.0000 | undef undef |
| Kidney | 0.0000 | 0.0000 | undef undef |
| Pancreas | 0.0000 | 0.0000 | undef undef |
| Prostate | 0.0033 | 0.0000 | undef 0.0000 |
| T lymphoma | 0.0047 | 0.0026 | 1.8089 0.5529 |
| Uterus | 0.0025 | 0.0000 | undef 0.0000 |
| White blood cells | 0.0031 | 0.0000 | undef 0.0000 |
| Hematopoietic | 0.0000 | 0.0000 | undef undef |
| Penis | 0.0027 | | |
| Seminal vesicle | 0.0000 | | |
| Sensory organs | 0.0000 | | |

FETUS % freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0000 |
| Brain | 0.0000 |
| Hematopoietic | 0.0039 |
| Skin | 0.0000 |
| Hepatic | 0.0260 |
| Heart-blood vessels | 0.0000 |
| Lung | 0.0000 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0000 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

| | |
|-------------------|--------|
| Breast | 0.0204 |
| Breast_t | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0110 |
| Gastrointestinal | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0000 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0000 |
| Nerves | 0.0040 |
| Kidney_t | 0.0000 |
| Ovary uterus | 0.0045 |
| Prostate_n | 0.0121 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |

Electronic Northern for Seq. ID: 401

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | 0.0125 | 0.0136 | 0.9198 1.0872 |
| Bladder | 0.0390 | 0.0094 | 4.1487 0.2410 |
| Breast | 0.0158 | 0.0056 | 2.8179 0.3549 |
| Large intestine | 0.0172 | 0.0028 | 6.0551 0.1652 |
| Small intestine | 0.0110 | 0.0000 | undef 0.0000 |
| Ovary | 0.0178 | 0.0119 | 1.4932 0.6697 |
| Endocrine tissue | 0.0161 | 0.0195 | 0.8231 1.2150 |
| Brain | 0.0179 | 0.0170 | 1.0581 0.9451 |
| Skin | 0.0220 | 0.0000 | undef 0.0000 |
| Hepatic | 0.0000 | 0.0000 | undef undef |
| Heart | 0.0162 | 0.0275 | 0.5907 1.6929 |
| Testicles | 0.0161 | 0.0000 | undef 0.0000 |
| Lung | 0.0175 | 0.0092 | 1.8944 0.5279 |
| Stomach-esophagus | 0.0000 | 0.0128 | 0.0000 undef |
| Muscle-skeleton | 0.0257 | 0.0037 | 6.9583 0.1437 |
| Kidney | 0.0201 | 0.0096 | 2.0891 0.4787 |
| Pancreas | 0.0066 | 0.0276 | 0.2393 4.1784 |
| Prostate | 0.0104 | 0.0000 | undef 0.0000 |
| T lymphoma | 0.0051 | 0.0448 | 0.1127 8.9727 |
| Uterus | 0.0177 | 0.0776 | 0.5426 1.5563 |
| White blood cells | 0.0116 | 0.0407 | 0.1916 5.2186 |
| Hematopoietic | 0.0040 | | |
| Penis | 0.0241 | | |
| Seminal vesicle | 0.0070 | | |
| Sensory organs | 0.0353 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0056 |
| Brain | 0.0000 |
| Hematopoietic | 0.0157 |
| Skin | 0.0000 |
| Hepatic | 0.0260 |
| Heart-blood vessels | 0.0036 |
| Lung | 0.0000 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0185 |
| Placenta | 0.1212 |
| Prostate | 0.0000 |
| Sensory organs | 0.0377 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0204 |
| Breast_t | 0.0000 |
| Large_intestine_t | 0.0000 |
| Ovary_n | 0.1595 |
| Ovary_t | 0.0253 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0226 |
| Gastrointestinal | 0.0122 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0324 |
| Testicles_n | 0.0167 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0000 |
| Lungs_t | 0.0000 |
| Nerves | 0.0191 |
| Kidney_t | 0.0000 |
| Ovary Uterus | 0.0248 |
| Prostate_n | 0.0061 |
| Sensory organs | 0.0077 |
| White blood cells | 0.0000 |

Electronic Northern for Seq. ID: 402

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | 0.0125 | 0.0000 | undef 0.0000 |
| Bladder | 0.0429 | 0.0141 | 3.0424 0.3287 |
| Breast | 0.0387 | 0.0084 | 4.5922 0.2178 |
| Large intestine | 0.0038 | 0.0028 | 1.3456 0.7432 |
| Small intestine | 0.0165 | 0.0107 | 1.5459 0.6469 |
| Ovary | 0.0237 | 0.0000 | undef 0.0000 |
| Endocrine tissue | 0.0177 | 0.0018 | 9.9589 0.1004 |
| Brain | 0.0041 | 0.0100 | 0.4062 2.4620 |
| Skin | 0.0514 | 0.0000 | undef 0.0000 |
| Hepatic | 0.0000 | 0.0063 | 0.0000 undef |
| Heart | 0.0457 | 0.0137 | 3.3227 0.3010 |
| Testicles | 0.0040 | 0.0000 | undef 0.0000 |
| Lung | 0.0467 | 0.0296 | 1.5786 0.6335 |
| Stomach-esophagus | 0.0145 | 0.0064 | 2.2671 0.4411 |
| Muscle-skeleton | 0.0171 | 0.0222 | 0.7731 1.2934 |
| Kidney | 0.0000 | 0.0000 | undef undef |
| Pancreas | 0.0017 | 0.0000 | undef 0.0000 |
| Prostate | 0.0075 | 0.0052 | 1.4470 0.6911 |
| T lymphoma | 0.0051 | 0.0000 | undef 0.0000 |
| Uterus | 0.0281 | 0.0138 | 2.0348 0.4915 |
| White blood cells | 0.0000 | 0.0000 | undef undef |
| Hematopoietic | 0.0160 | | |
| Penis | 0.0293 | | |
| Seminal vesicle | 0.0141 | | |
| Sensory organs | 0.0353 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0418 |
| Gastrointestinal | 0.0139 |
| Brain | 0.0000 |
| Hematopoietic | 0.0039 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0356 |
| Lung | 0.0325 |
| Adrenal gland | 0.0000 |
| Kidney | 0.0124 |
| Placenta | 0.0121 |
| Prostate | 0.0249 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0476 |
| Breast_t | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n | 0.1595 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0220 |
| Gastrointestinal | 0.0122 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0583 |
| Testicles_n | 0.0042 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0098 |
| Lungs_t | 0.0000 |
| Nerves | 0.0090 |
| Kidney_t | 0.0000 |
| Ovary uterus | 0.0405 |
| Prostate_n | 0.0061 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |

Electronic Northern for Seq. ID: 403

| | NORMAL % freq. | TUMOR % freq. | RATIOS N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma | 0.0000 | 0.0000 | undef undef |
| Bladder | 0.0351 | 0.0047 | 7.4677 0.1339 |
| Breast | 0.0070 | 0.0014 | 5.0097 0.1396 |
| Large intestine | 0.0115 | 0.0000 | undef 0.0000 |
| Small intestine | 0.0000 | 0.0000 | undef undef |
| Ovary | 0.0000 | 0.0024 | 0.0000 undef |
| Endocrine tissue | 0.0016 | 0.0035 | 0.4527 2.2091 |
| Brain | 0.0017 | 0.0060 | 0.2901 3.4467 |
| Skin | 0.0000 | 0.0000 | undef undef |
| Hepatic | 0.0000 | 0.0063 | 0.0000 undef |
| Heart | 0.0020 | 0.0137 | 0.1477 6.7715 |
| Testicles | 0.0040 | 0.0000 | undef 0.0000 |
| Lung | 0.0039 | 0.0013 | 2.1049 0.4751 |
| Stomach-esophagus | 0.0145 | 0.0000 | undef 0.0000 |
| Muscle-skeleton | 0.0051 | 0.0000 | undef 0.0000 |
| Kidney | 0.0112 | 0.0000 | undef 0.0000 |
| Pancreas | 0.0017 | 0.0055 | 0.2992 3.3427 |
| Prostate | 0.0075 | 0.0026 | 2.8941 0.3455 |
| T lymphoma | 0.0025 | 0.0000 | undef 0.0000 |
| Uterus | 0.0059 | 0.0046 | 1.2851 0.7781 |
| White blood cells | 0.0027 | 0.0000 | undef 0.0000 |
| Hematopoietic | 0.0013 | | |
| Penis | 0.0054 | | |
| Seminal vesicle | 0.0000 | | |
| Sensory organs | 0.0000 | | |

FETUS
% freq.

| | |
|---------------------|--------|
| Development | 0.0000 |
| Gastrointestinal | 0.0000 |
| Brain | 0.0039 |
| Hematopoietic | 0.0000 |
| Skin | 0.0000 |
| Hepatic | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung | 0.0254 |
| Adrenal gland | 0.0185 |
| Kidney | 0.0121 |
| Placenta | 0.0000 |
| Prostate | 0.0000 |
| Sensory organs | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

| | |
|-------------------|--------|
| Breast | 0.0340 |
| Breast_t | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n | 0.0000 |
| Ovary_t | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal | 0.0017 |
| Gastrointestinal | 0.0000 |
| Hematopoietic | 0.0000 |
| Skin-muscle | 0.0065 |
| Testicles_n | 0.0000 |
| Testicles_t | 0.0000 |
| Lungs_n | 0.0098 |
| Lungs_t | 0.0000 |
| Nerves | 0.0020 |
| Kidney_t | 0.0000 |
| Ovary uterus | 0.0000 |
| Prostate_n | 0.0061 |
| Sensory organs | 0.0000 |
| White blood cells | 0.0000 |

2.2. Fisher Test

In order to decide whether a partial sequence S of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to S . If the null hypothesis can be rejected with high enough certainty, the gene belonging to S is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

Example 3

Automatic Lengthening of the Partial Sequence

Automatic lengthening of partial sequence S is completed in three steps:

1. Determination of all sequences homologous to S from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence C from the assembled sequences.

Consensus sequence C will generally be longer than initial sequence S . Its electronic Northern Blot will accordingly

deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences C_i (i : iteration index) obtained in each case until the alternative hypothesis is rejected (if H_0 Exit; truncation criterion I) or until automatic lengthening is no longer possible (while $C_i > C_{i-1}$; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from normal bladder tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORF's) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

Example 4

Mapping of Nucleic Acid Sequences on the Human Genome

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server (http://www.stanford.edu/RH/rhserver_form2.html). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "MapView" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the Gap between Genome Mapping and Genome Sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence Mapping by Electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

the results were evaluated with the above-mentioned software and the software of the Whitehead Institute (<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

Example 5

Obtaining genomic DNA sequences (BAC clones)

The genomic BAC clones containing the corresponding cDNAs (<http://www.tree.caltech.edu/>; Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797) were isolated with the procedure of "down-to-the-well". In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is moved into a certain raster, so that the DNA of these clones with a specific PCR can be studied. In doing so, "pooling" of the DNA of different BAC clones takes place. Combinatorial analysis makes it possible to determine the clones that contain the desired DNA. By fixing the clones, the address of the clones in the library can be determined. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

The libraries used were CITB B and CITB C:

| Seq. ID No. | Identified BACs | | |
|-------------|-----------------|----------|----------|
| 60 | 311/K/13 | 271/E/3 | 252/P/20 |
| 102 | 458/N/24 | 349/F/12 | |

TABLE I

Col. 1 - Sequence ID

Col. 2 - Expression

Col. 3 - Function

Col. 4 - Modules

Col. 5 - Cytogenetic localization

Col. 6 - Nearest marker

TABLE I

| Sequence ID | Expression | Function |
|-------------|----------------------------------------|-----------------------------------------------------------|
| 1 | Overexpressed in normal bladder tissue | H. sapiens rap1b |
| 2 | Overexpressed in normal bladder tissue | Human zinc finger transcription factor hEZF (EZF) homolog |
| 3 | Overexpressed in normal bladder tissue | Homo sapiens mRNA for phosphatidic acid phosphatase 2a |
| 4 | Overexpressed in normal bladder tissue | H. sapiens mRNA for G protein-coupled receptor Edg-2 |
| 6 | Overexpressed in normal bladder tissue | Homo sapiens secreted frizzled-related protein |
| 7 | Overexpressed in normal bladder tissue | Human monocytic leukemia zinc finger protein (MOZ) |
| 4 | Overexpressed in normal bladder tissue | Homo sapiens angiotensin II receptor |
| 6 | Overexpressed in normal bladder tissue | Human mRNA for RNA helicase (HRH1) |
| 12 | Overexpressed in normal bladder tissue | H. sapiens rhoB |
| 13 | Overexpressed in normal bladder tissue | Human skeletal muscle LIM-protein SLIM 1 |
| 14 | Overexpressed in normal bladder tissue | Homo sapiens 39 kDa protein |
| 17 | Overexpressed in normal bladder tissue | H. sapiens dermatopontin mRNA |
| 18 | Overexpressed in normal bladder tissue | Homo sapiens phosphoglucomutase-related protein (PGMRP) |

| | | |
|----|----------------------------------------------|---------------------------------------------------|
| 20 | Overexpressed in normal bladder tissue | Human nucleic acid binding protein CNBP |
| 21 | Overexpressed in normal bladder tissue | Unknown |
| 22 | Overexpressed in normal bladder tissue | Human small nuclear ribonucleoprotein (U1-70K) |
| 23 | Overexpressed in normal bladder tissue | H. sapiens mRNA for telokin homolog |
| 24 | Overexpressed in normal bladder tissue | Homologous to pil2 from rats |
| 25 | Overexpressed in normal bladder tissue | Unknown |
| 26 | Overexpressed in normal bladder tissue | Unknown |
| 27 | Overexpressed in normal bladder tissue | Unknown |
| 29 | Overexpressed in normal bladder tissue | Homologous to sushi repeat protein |
| 30 | Overexpressed in normal bladder tissue | Unknown |
| 31 | Overexpressed in normal bladder tissue | Unknown |
| 32 | Overexpressed in normal bladder tissue | Unknown |
| 33 | Overexpressed in normal bladder tissue | Unknown |
| 34 | Overexpressed in normal bladder tissue | Unknown |

| | | |
|----|----------------------------------------------|-----------------------------------------------------------------------|
| 35 | Overexpressed in normal bladder tissue | Caenorhabditis elegans cosmid F09E5 |
| 36 | Overexpressed in normal bladder tissue | Unknown |
| 37 | Overexpressed in normal bladder tissue | Homologous to murine RING zinc finger protein |
| 38 | Overexpressed in normal bladder tissue | Rattus norvegicus cytoplasmic dynein intermediate chain 2c |
| 39 | Overexpressed in normal bladder tissue | Unknown |
| 40 | Overexpressed in normal bladder tissue | Unknown |
| 43 | Overexpressed in normal bladder tissue | Gry-rbp |
| 44 | Overexpressed in normal bladder tissue | Unknown |
| 46 | Overexpressed in normal bladder tissue | Unknown |
| 47 | Overexpressed in normal bladder tissue | Unknown |
| 48 | Overexpressed in normal bladder tissue | Unknown |
| 50 | Overexpressed in normal bladder tissue | Homologous to HU-K5 |
| 51 | Overexpressed in normal bladder tissue | Unknown |
| 52 | Overexpressed in normal bladder tissue | Homologous to O. aries putative G- protein linked receptor (edg-2) |

| | | |
|----|----------------------------------------------|-----------------------------------------------------------------|
| 53 | Overexpressed in normal bladder tissue | Unknown |
| 54 | Overexpressed in normal bladder tissue | Human homolog to murine NST-1 |
| 55 | Overexpressed in normal bladder tissue | Homologous to human CIP4 |
| 56 | Overexpressed in normal bladder tissue | Human Chf5p homolog |
| 57 | Overexpressed in normal bladder tissue | Unknown |
| 58 | Overexpressed in normal bladder tissue | Unknown |
| 59 | Overexpressed in normal bladder tissue | Unknown |
| 60 | Overexpressed in normal bladder tissue | Unknown |
| 61 | Overexpressed in normal bladder tissue | Caenorhabditis elegans cosmid TC9A5 |
| 62 | Overexpressed in normal bladder tissue | Unknown |
| 63 | Overexpressed in normal bladder tissue | Unknown |
| 65 | Overexpressed in normal bladder tissue | Homologous to human KOX15 |
| 67 | Overexpressed in normal bladder tissue | Unknown |
| 69 | Overexpressed in normal bladder tissue | Homologous to Golgi 4-transmembrane spanning transporter MTP |

| | | |
|----|----------------------------------------------|---------------------------------------------------|
| 72 | Overexpressed in normal bladder tissue | Unknown |
| 73 | Overexpressed in normal bladder tissue | Unknown |
| 75 | Overexpressed in normal bladder tissue | Human homolog to rat mRNA for V-1 protein |
| 77 | Overexpressed in normal bladder tissue | Caenorhabditis elegans cosmid F 13G3 |
| 78 | Overexpressed in normal bladder tissue | Unknown |
| 79 | Overexpressed in normal bladder tissue | Unknown |
| 80 | Overexpressed in normal bladder tissue | Human pyruvate dehydrogenase kinase isoform 4 |
| 82 | Overexpressed in normal bladder tissue | Unknown |
| 83 | Overexpressed in normal bladder tissue | Unknown |
| 85 | Overexpressed in normal bladder tissue | Unknown |
| 86 | Overexpressed in normal bladder tissue | Mouse epithelial zinc-finger protein EZF (Zie) |
| 88 | Overexpressed in normal bladder tissue | Unknown |
| 90 | Overexpressed in normal bladder tissue | Unknown |
| 92 | Overexpressed in normal bladder tissue | Homologous to MyD118 |

| | | |
|-----|----------------------------------------------|------------------------------------------------------|
| 93 | Overexpressed in normal bladder tissue | Homologous to p8 protein from rats |
| 94 | Overexpressed in normal bladder tissue | Unknown |
| 95 | Overexpressed in normal bladder tissue | Unknown |
| 96 | Overexpressed in normal bladder tissue | Homologous to murine B-1ND1 |
| 97 | Overexpressed in normal bladder tissue | Canis familiaris Sec61-complex gamma-subunit |
| 98 | Overexpressed in normal bladder tissue | Unknown |
| 99 | Overexpressed in normal bladder tissue | Human homolog to X taevis 146 kDa nuclear protein |
| 100 | Overexpressed in normal bladder tissue | Unknown |
| 101 | Overexpressed in normal bladder tissue | Human dysferlin |
| 102 | Overexpressed in normal bladder tissue | Unknown |
| 103 | Overexpressed in normal bladder tissue | Unknown |
| 104 | Overexpressed in normal bladder tissue | Unknown |
| 105 | Overexpressed in normal bladder tissue | Unknown |
| 106 | Overexpressed in normal bladder tissue | Unknown |

| | | |
|-----|----------------------------------------------|-------------------------------------------|
| 107 | Overexpressed in normal bladder tissue | Unknown |
| 108 | Overexpressed in normal bladder tissue | Homologous to APRIL |
| 109 | Overexpressed in normal bladder tissue | Homologous to the human p20 |
| 110 | Overexpressed in normal bladder tissue | Unknown |
| 111 | Overexpressed in normal bladder tissue | Unknown |
| 112 | Overexpressed in normal bladder tissue | Unknown |
| 113 | Overexpressed in normal bladder tissue | Homologous to D. melanogaster furrowed |
| 114 | Overexpressed in normal bladder tissue | Homologous to murine BRX protein |
| 115 | Overexpressed in normal bladder tissue | Unknown |
| 116 | Overexpressed in normal bladder tissue | Unknown |
| 117 | Overexpressed in normal bladder tissue | Caenorhabditis elegans cosmid R08D7 |
| 118 | Overexpressed in normal bladder tissue | Unknown |
| 119 | Overexpressed in normal bladder tissue | HSP 86 |
| 120 | Overexpressed in normal bladder tissue | Homologous to human AKAP95 |

| | | |
|-----|----------------------------------------|----------------------------------------------------------------------|
| 121 | Overexpressed in normal bladder tissue | Sus scrofa mRNA for 17-kDa PKC-potentiated inhibitory protein of PP1 |
| 122 | Overexpressed in normal bladder tissue | Unknown |
| 123 | Overexpressed in normal bladder tissue | Homo sapiens supervillin |
| 124 | Overexpressed in normal bladder tissue | Homologous to B. taurus vacuolar ATPase subunit A |
| 125 | Overexpressed in normal bladder tissue | SH3 domain binding glutamic acid-rich-like protein |
| 126 | Overexpressed in normal bladder tissue | Human homolog to Mus musculus WSB-1 |
| 127 | Overexpressed in normal bladder tissue | Unknown |
| 391 | Lengthening to Seq. ID No: 27 | |
| 392 | Lengthening to Seq. ID No: 34 | |
| 393 | Lengthening to Seq. ID No: 50 | |
| 394 | Lengthening to Seq. ID No: 56 | |
| 395 | Lengthening to Seq. ID No: 78 | |
| 396 | Lengthening to Seq. ID No: 82 | |
| 397 | Lengthening to Seq. ID No: 88 | |
| 398 | Lengthening to Seq. ID No: 100 | |
| 399 | Lengthening to Seq. ID No: 101 | |

| | | |
|-----|--------------------------------------|--|
| 400 | Lengthening to Seq. ID No: 102 | |
| 401 | Lengthening to Seq. ID No: 104 | |
| 402 | Lengthening to Seq. ID No: 110 | |
| 403 | Lengthening to Seq. ID No: 111 | |

[Key to Table I:]

[Column 4: Sequence ID No. 109:] crystallin = crystalline

[Column 6: Sequence ID Nos. 6, 7, 9, 22, 29, 31-34, 39, 43, 46,
48, 50, 51, 56, 58-62, 65, 72, 73, 82, 86, 102,
103, 111, 112, 115, 126:] ... bis ... = ... to ...

TABELLE I

| Sequenz ID | Expression | Funktion | Module | Cytogenetische Lokalisation | Nearest Marker |
|------------|--------------------------------------|-----------------------------------------------------------|--------------------------------|-----------------------------|---------------------------|
| 1 | in Blasennormalgewebe überexprimiert | H sapiens rap1b | ras | 6q21-q22.1 | D6S304-D6S1639 |
| 2 | in Blasennormalgewebe überexprimiert | Human zinc finger transcription factor HEZF (EZF) Homolog | ZINC_FINGER_C2H2_2 | | |
| 3 | in Blasennormalgewebe überexprimiert | Homo sapiens mRNA for phosphatidic acid phosphatase 2a | | | |
| 4 | in Blasennormalgewebe überexprimiert | H sapiens mRNA for G protein-coupled receptor Edg-2 | 7tm_1 | 9q31.3-q32 | D9S1690-D9S279 |
| 6 | in Blasennormalgewebe überexprimiert | Homo sapiens secreted frizzled-related protein | FZ_DOMAIN; NETRIN_CT; PRO_RICH | 8p11.23-p12 | SHGC-5722 bis SHGC-5765 |
| 7 | in Blasennormalgewebe überexprimiert | Human monocytic leukaemia zinc finger protein (MOZ) | | 8p11.23-p12 | D8S2070 bis SHGC-31558 |
| 8 | in Blasennormalgewebe überexprimiert | Homo Sapiens angiotensin II receptor | | 22q11.22-q11.23 | D6S2136-D4S3274 |
| 9 | in Blasennormalgewebe überexprimiert | Human mRNA for RNA helicase (HRH1) | | 6p21.31 | SHGC-17229 bis D6S478 |
| 12 | in Blasennormalgewebe überexprimiert | H sapiens rhoB | | 2p23.3 | D2S387 |
| 13 | in Blasennormalgewebe überexprimiert | Human skeletal muscle LIM-protein SLIM1 | LIM_DOMAIN_2 | Xq25-q27.2 | DXS994-DXS1062 |
| 14 | in Blasennormalgewebe überexprimiert | Homo sapiens 39 kDa protein | PDZ; LIM | 4q34.1-q35.2 | D4S408-D4S426 |
| 17 | in Blasennormalgewebe überexprimiert | H sapiens dermatopontin mRNA | | 1q23.1-q23.2 | D1S445-D1S2750 |
| 18 | in Blasennormalgewebe überexprimiert | Homo sapiens phosphoglucomutase-related protein (PGMRP) | PGM_PMM | 9p11.1-q12 | D9S1699 |
| 20 | in Blasennormalgewebe überexprimiert | Human nucleic acid binding protein CNBP | ZfCCHC | 3q13.31-q21.1 | D3S1589-D3S1766 |
| 21 | in Blasennormalgewebe überexprimiert | unbekannt | | | |
| 22 | in Blasennormalgewebe überexprimiert | Human small nuclear ribonucleoprotein (U1-70K) | | 19q13.31-q13.33 | SHGC-36947 bis SHGC-34723 |
| 23 | in Blasennormalgewebe überexprimiert | H sapiens mRNA for telokin Homolog | | | |
| 24 | in Blasennormalgewebe überexprimiert | Homolog zu p12 aus Ratte | | | |

| Sequenz ID | Expression | Funktion | Module | Cytogenetische Lokalisation | Nearest Marker |
|------------|--------------------------------------|------------------------------------------------------------|-------------------|-----------------------------|---------------------------|
| 25 | in Blasennormalgewebe überexprimiert | unbekannt | | | |
| 26 | in Blasennormalgewebe überexprimiert | unbekannt | | | |
| 27 | in Blasennormalgewebe überexprimiert | unbekannt | | 5q32-q33.1 | D5S470 |
| 29 | in Blasennormalgewebe überexprimiert | Homolog zu susII repeat protein | PRO_RICH | 3q11.2 | SHGC-36351 bis SHGC-14633 |
| 30 | in Blasennormalgewebe überexprimiert | unbekannt | | 2q37.3 | D2S206-D2S331 |
| 31 | in Blasennormalgewebe überexprimiert | unbekannt | | 2q31.1-q31.3 | W1-7596 bis D2S326 |
| 32 | in Blasennormalgewebe überexprimiert | unbekannt | | 20p13 | D20S864 bis SHGC-34269 |
| 33 | in Blasennormalgewebe überexprimiert | unbekannt | | 13q12.11-q12.3 | SHGC-2665 bis D13S289 |
| 34 | in Blasennormalgewebe überexprimiert | unbekannt | | 9q21.31 | SHGC-32247 bis SHGC-5528 |
| 35 | in Blasennormalgewebe überexprimiert | Caenorhabditis elegans cosmid F09E5 | UPF0001 | | |
| 36 | in Blasennormalgewebe überexprimiert | unbekannt | | | |
| 37 | in Blasennormalgewebe überexprimiert | Homolog zu murinem RING zinc finger protein | PRO_RICH; ZF_RING | 17p13.3 | D17S1548 |
| 38 | in Blasennormalgewebe überexprimiert | Rattus norvegicus cytoplasmic dynein intermediate chain 2c | WD40_REGION | 10q11.21 | D10S804-D10S220 |
| 39 | in Blasennormalgewebe überexprimiert | unbekannt | | 13q33.3 | SHGC-9496 bis D13S1223 |
| 40 | in Blasennormalgewebe überexprimiert | unbekannt | | | |
| 43 | in Blasennormalgewebe überexprimiert | Gry-rbp | RBD | 20p13 | D20S816 bis SHGC-33687 |
| 44 | in Blasennormalgewebe überexprimiert | unbekannt | | | |
| 46 | in Blasennormalgewebe überexprimiert | unbekannt | f. | 2q21.3-q22.1 | SHGC-35092 bis SHGC-32856 |
| 47 | in Blasennormalgewebe überexprimiert | unbekannt | | | |

X09000-14882960

| Sequenz ID | Expression | Funktion | Module | Cytogenetische Lokalisation | Nearest Marker |
|------------|--------------------------------------|----------------------------------------------------------------|--------------------|-----------------------------|---------------------------|
| 48 | in Blasennormalgewebe überexprimiert | unbekannt | | 15q11.2-q15.3 | SHGC-35142 bis SHGC-7407 |
| 50 | in Blasennormalgewebe überexprimiert | Homolog zu HU-K5 | | 3q21.3-3q23 | SHGC-37132 bis SHGC-30693 |
| 51 | in Blasennormalgewebe überexprimiert | unbekannt | | 3p21.31-p21.1 | SHGC-30574 bis SHGC-31529 |
| 52 | in Blasennormalgewebe überexprimiert | Homolog zu O. aries Putative G-protein linked receptor (edg-2) | | | |
| 53 | in Blasennormalgewebe überexprimiert | unbekannt | | | |
| 54 | in Blasennormalgewebe überexprimiert | Humanes Homolog zu murinem NST-1 | HSP70 | | |
| 55 | in Blasennormalgewebe überexprimiert | Homolog zu humanem CIP4 | | | |
| 56 | in Blasennormalgewebe überexprimiert | Humanes Cbl5p Homolog | | Xq25-q27.3 | SHGC-31168 bis AFM207xb8 |
| 57 | in Blasennormalgewebe überexprimiert | unbekannt | ZF_DHHG; NLS_BP | | |
| 58 | in Blasennormalgewebe überexprimiert | unbekannt | | 9q12 | WI-7387 bis SHGC-32868 |
| 59 | in Blasennormalgewebe überexprimiert | unbekannt | | 9q22.2-q22.31 | SHGC-14680 bis SHGC-8725 |
| 60 | in Blasennormalgewebe überexprimiert | unbekannt | | 1p36.13-p36.31 | SHGC-34104 bis SHGC-9861 |
| 61 | in Blasennormalgewebe überexprimiert | Caenorhabditis elegans cosmid T09A5 | | Chr.5 | SHGC-21758 bis SHGC-4278 |
| 62 | in Blasennormalgewebe überexprimiert | unbekannt | | 1q32.3 | SHGC-15949 bis SHGC-11476 |
| 63 | in Blasennormalgewebe überexprimiert | unbekannt | Oxysterol_BP | 1p32.3-p33 | D1S197 D1S417 |
| 65 | in Blasennormalgewebe überexprimiert | Homolog zu humanem KOX15 | ZINC_FINGER_C2H2_2 | 16q21-q23.1 | D16S2624 bis SHGC-9008 |
| 67 | in Blasennormalgewebe überexprimiert | unbekannt | | | |
| 69 | in Blasennormalgewebe überexprimiert | Homolog zu Golgi 4-Transmembran spanning Transporter MTP | | 8q22.3-q24.13 | D6S556 D6S266 |
| 72 | in Blasennormalgewebe überexprimiert | unbekannt | | 10q23.1 | SHGC-14535 bis SHGC-30780 |

| Sequenz ID | Expression | Funktion | Module | Cytogenetische Lokalisation | Nearest Marker |
|------------|--------------------------------------|-------------------------------------------------|---------------|-----------------------------|---------------------------|
| 73 | in Blasennormalgewebe überexprimiert | unbekannt | | 1q22 | SHGC-32839 bis DIS1576 |
| 75 | in Blasennormalgewebe überexprimiert | Humanes Homolog zu Rat mRNA for V-ank 1 protein | | | |
| 77 | in Blasennormalgewebe überexprimiert | Caenorhabditis elegans cosmid F13G3 | Ribosomal_L13 | 8q23.3-q24.11 | WI-5098-CHLC.GATA8G03.443 |
| 78 | in Blasennormalgewebe überexprimiert | unbekannt | lg | | |
| 79 | in Blasennormalgewebe überexprimiert | unbekannt | | | |
| 80 | in Blasennormalgewebe überexprimiert | Humane Pyruvate Dehydrogenase Kinase Isoform 4 | | 7q21.2-q22.1 | D7S482-D7S662 |
| 82 | in Blasennormalgewebe überexprimiert | unbekannt | | 3p24.3-p23 | SHGC-9648 bis SHGC-14769 |
| 83 | in Blasennormalgewebe überexprimiert | unbekannt | | 3p12.1-p21.1 | D3S3117 |
| 85 | in Blasennormalgewebe überexprimiert | unbekannt | | | |
| 86 | in Blasennormalgewebe überexprimiert | Mouse epithelial zinc-finger protein EZF (Zie) | | 9q22.33-q31.1 | D9S1690 bis SHGC-14345 |
| 88 | in Blasennormalgewebe überexprimiert | unbekannt | | 1p35.1 | D1S2569-D1S2676 |
| 90 | in Blasennormalgewebe überexprimiert | unbekannt | | | |
| 92 | in Blasennormalgewebe überexprimiert | Homolog zu MyD118 | | | |
| 93 | in Blasennormalgewebe überexprimiert | Homolog zum p8 Protein aus Ratte | ras | 16p11.2-q12.1 | D16S3093-D16S409 |
| 94 | in Blasennormalgewebe überexprimiert | unbekannt | | 14q11.1-q11.2 | D14S990-D14S264 |
| 95 | in Blasennormalgewebe überexprimiert | unbekannt | | 16p13.2-p13.3 | D16S521 |
| 96 | in Blasennormalgewebe überexprimiert | Homolog zu murinem B-IND1 | | 15q22.31-q22.33 | D15S159-D15S125 |
| 97 | in Blasennormalgewebe überexprimiert | Canis familiaris Sec61-complex gamma-subunit | SecE | | |
| 98 | in Blasennormalgewebe überexprimiert | unbekannt | | 6p21.2-p21.31 | D6S276-D6S439 |

| Sequenz ID | Expression | Funktion | Module | Cytogenetische Lokalisation | Nearest Marker |
|------------|--------------------------------------|---------------------------------------------------------------|-----------------------|-----------------------------|---------------------------|
| 99 | in Blasennormalgewebe überexprimiert | Humanes Homolog zu X laevis 146 kDa nuclear protein unbekannt | | 2q23.3-q33.3 | D2S117-D2S115 |
| 100 | in Blasennormalgewebe überexprimiert | | NLS_BP | 9q22.31-q31.1 | D9S176-D9S277 |
| 101 | in Blasennormalgewebe überexprimiert | Humanes Dysferlin | PRO_RICH; C2_DOMAIN_2 | | |
| 102 | in Blasennormalgewebe überexprimiert | unbekannt | | 10q25.3 | D10S216 bis SHGC-13289 |
| 103 | in Blasennormalgewebe überexprimiert | unbekannt | | 2p23.1-p23.2 | D2S2573 bis SHGC-16275 |
| 104 | in Blasennormalgewebe überexprimiert | unbekannt | PRO_RICH | 8p11.23-p12 | D8S2102 |
| 105 | in Blasennormalgewebe überexprimiert | unbekannt | | 1p31.1-p34.1 | SHGC-32050 |
| 106 | in Blasennormalgewebe überexprimiert | unbekannt | | 13q21.33-q22.1 | D13S156-D13S162 |
| 107 | in Blasennormalgewebe überexprimiert | unbekannt | | | |
| 108 | in Blasennormalgewebe überexprimiert | Homolog zu APRIL | TNF | | |
| 109 | in Blasennormalgewebe überexprimiert | Homolog zu dem humanem p20 | crystallin; HSP20 | 19q13.13 | D19S425-D19S224 |
| 110 | in Blasennormalgewebe überexprimiert | unbekannt | | 7q31.31 | D7S522-D7S2756 |
| 111 | in Blasennormalgewebe überexprimiert | unbekannt | | 10q23.31-q24.1 | WI-7908 bis SHGC-34547 |
| 112 | in Blasennormalgewebe überexprimiert | unbekannt | | 1q31.1-q31.3 | SHGC-34113 bis SHGC-34344 |
| 113 | in Blasennormalgewebe überexprimiert | Homolog zu D. melanogaster furrowed | sushi | 9q31.3-q32 | D9S160-D9S279 |
| 114 | in Blasennormalgewebe überexprimiert | Homolog zu murinem BRX Protein | PRO_RICH | | |
| 115 | in Blasennormalgewebe überexprimiert | unbekannt | | Chr. 17 (17p13.3-q25.3) | SHGC-33067 bis SHGC-32338 |
| 116 | in Blasennormalgewebe überexprimiert | unbekannt | | 4q28.1-q31.1 | D4S1580-D4S427 |
| 117 | in Blasennormalgewebe überexprimiert | Caenorhabditis elegans cosmid R08D7 | | | |

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| Sequenz ID | Expression | Funktion | Module | Cytogenetische Lokalisation | Nearest Marker |
|------------|--------------------------------------|----------------------------------------------------------------------|--------------------------------|-----------------------------|------------------------|
| 118 | in Blasennormalgewebe überexprimiert | unbekannt | PRO_RICH | | |
| 119 | in Blasennormalgewebe überexprimiert | HSP 86 | HSP90 | 11q13.2-q13.5 | D11S913-D11S1314 |
| 120 | in Blasennormalgewebe überexprimiert | Homolog zu humanem AKAP95 | PRO_RICH | | |
| 121 | in Blasennormalgewebe überexprimiert | Sus scrofa mRNA for 17-kDa PKC-potentiated inhibitory protein of PP1 | PRO_RICH | 19q13.13-q13.2 | D19S1069-D19S421 |
| 122 | in Blasennormalgewebe überexprimiert | unbekannt | | 1q32.1 | D1S306-D1S2570 |
| 123 | in Blasennormalgewebe überexprimiert | Homo sapiens Supervillin | PRO_RICH | | |
| 124 | in Blasennormalgewebe überexprimiert | Homolog zu B laurus vacuolar ATPase subunit A | | 3q11.2-q21.1 | D3S2353-D3S3526 |
| 125 | in Blasennormalgewebe überexprimiert | SH3 domain binding glutamic acid-rich-like protein | | domain | binding |
| 126 | in Blasennormalgewebe überexprimiert | Humanes Homolog zu Mus musculus WSB-1 | WD40_REGION; WD40; SOCS_DOMAIN | 17p11.2 | D17S783 bis SHGC-30289 |
| 127 | in Blasennormalgewebe überexprimiert | unbekannt | | | |
| 391 | Verlängerung zu Seq ID No: 27 | | | | |
| 392 | Verlängerung zu Seq ID No: 34 | | | | |
| 393 | Verlängerung zu Seq ID No: 50 | | | | |
| 394 | Verlängerung zu Seq ID No: 56 | | | | |
| 395 | Verlängerung zu Seq ID No: 78 | | | | |
| 396 | Verlängerung zu Seq ID No: 82 | | | | |
| 397 | Verlängerung zu Seq ID No: 88 | | | | |
| 398 | Verlängerung zu Seq ID No: 100 | | | | |
| 399 | Verlängerung zu Seq ID No: 101 | | | | |

| Sequenz ID | Expression | Funktion | Module | Cytogenetische Lokalisation | Nearest Marker |
|------------|--------------------------------|----------|--------|-----------------------------|----------------|
| 400 | Verlängerung zu Seq ID No. 102 | | | | |
| 401 | Verlängerung zu Seq ID No. 104 | | | | |
| 402 | Verlängerung zu Seq ID No. 110 | | | | |
| 403 | Verlängerung zu Seq ID No. 111 | | | | |

TABLE II

Seq. ID No. Peptide Sequences (ORF's) Seq. ID. No.

| Seq. ID. No. | Peptid-Sequenzen (ORF's) | Seq. ID. No. |
|--------------|--------------------------|--------------|
| 21 | | 430 |
| | | 431 |
| 24 | | 128 |
| | | 129 |
| 25 | | 131 |
| | | 132 |
| | | 133 |
| 26 | | 134 |
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| 27 | | 137 |
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| 29 | | 143 |
| 30 | | 144 |
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| 37 | | 167 |
| 38 | | 168 |
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| 40 | | 172 |
| | | 173 |
| | | 174 |
| 43 | | 181 |
| 44 | | 182 |
| | | 183 |
| | | 184 |

Seq. ID No.

Peptide Sequences (ORF's) Seq. ID. No.

| Seq. ID. No. | Peptid-Sequenzen (ORF's) | Seq. ID. No. |
|--------------|--------------------------|--------------|
| 46 | | 188 |
| | | 189 |
| | | 190 |
| 47 | | 191 |
| | | 192 |
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| 48 | | 194 |
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| 69 | | 243 |
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| 75 | | 260 |
| 77 | | 264 |

Seq. ID No.

Peptide Sequences (ORF's) Seq. ID. No.

| Seq. ID. No. | Peptid-Sequenzen (ORF's) | Seq. ID. No. |
|--------------|--------------------------|--------------|
| 78 | | 265 |
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|Peptid-Sequenzen (ORF's) Seq. ID. No.

397

Seq. ID No. Peptide Sequences (ORF's) Seq. ID. No.

| Seq. ID. No. | Peptid-Sequenzen (ORF's) | Seq. ID. No. |
|--------------|--------------------------|--------------|
| 126 | | 388 |
| 127 | | 389 |
| | | 390 |
| 391 | | 404 |
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| 401 | | 424 |
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| 402 | | 426 |
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| 403 | | 428 |
| | | 429 |

The inventive nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of the determined candidate genes and the determined amino acid sequences Seq. ID Nos. 128-390 and 404-431 are described in the following sequence protocol.

Sequence Protocol**(1) GENERAL INFORMATION:****(i) APPLICANT:**

- (A) NAME: metaGen - Gesellschaft für Genomforschung mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Normal Bladder Tissue**(iii) Number of sequences: 365****(iv) COMPUTER-READABLE FORM:**

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)

(2) INFORMATION ON SEQ ID NO. 1:**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 1722 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing**(iii) HYPOTHETICAL: NO****(iii) ANTI-SENSE: NO****(vi) ORIGIN:**

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

cgttgaagta gatgcacaac agtgtatgct tgaatcttgc gatactgcag gaacggagca 60
atttacagca atgaggggatt tatacatgaa aaatggacaa ggatttgcatt tagtttattc 120
catcacagca cagtccacat ttaacgattt acaagacctg agagaacaga ttcttcgagt 180

taaaagacact gatgatgttc caatgatctt tgttggtaat aagtgtgact tgggaagatga 240
aagagttgtta ggggaaggaa aaggtcaaaa tctagcaaga caatgggaaca actgtgcatc 300
cttagaattct tctgcataaa caaaaataaa tgttaatgag atctttttatg acctagtgcg 360
gcaaatatac agaaaaaaccc cagtgcctgg gaaggctcgc aaaaagtcac catgtcagct 420
gcttttaatar actaaatgca ttgtagctct gagccaggtc tgaagaactg ttgcccaatt 480
caacagtgcc agcattccaa ctttgttaaa cctaccaaca tcttaaatgg accttccctgt 540
ggtgggtaccc ttttaagaggc ggaatgaaagc tactatatca gtttgcacat tctaatcact 600
ttccagtatc acaagagaga tttttactta tataatagtc ctgaggtttg cagctgggtaa 660
aacCagaggc tacatccagt attactgcta agagacattc ttcatccacc aatgttgtag 720
atgtatgaaa atgggtgtact gtataccttta acatgcccca tactttgtat tggagagtag 780
aataatgttaa atcctaaaaag caccactatt ttagcataat aaaaagaagt ccaaaagagct 840
cctatataga ctactccaga taacttcgct tctttgatac ttgtagctta ttgttaatttt 900
ttttaagaaa tccaagggtca ttattattgt acaaaaataag cgctttgatt aacacagcta 960
tatagttttt ttaatttttta aaaaacctgt ggagacgggt atcttgcctt taaaacatga1020
tagtcccttc agtataatgt cttagattaa agacgttgcc ttttaatatc gttgggaagg1080
aaatgtccag acttttccaa tctcttatta tatgtttcct ttttttggtt acatagggga1140
caatgtttat agtctgtgtg acagtggggg totacaacaa gaagtgtata ttttcaaaal200
atttttttaat gatttaacaa tttttgtaaa tcattttcag gcttctgcag ctgtagattc1260
tcactgtgaa tcccttgctc gctcatgcac aagtgtattt gcaataccaa atatacaggt1320
ttagtatttt tgcctgttag tgattgtttc acatgtgtaa cgtttttggtt gagatgttaa1380
atgggtgcag agtactgttg atgtgaatgt gggaagtaat ttttaatcata tgtaattgggt1440
cacaaggcct aatttgcagt aactattgct gttttattta acaatgcctt gttgctttgt1500
atgcattaat gtttggagct aaagattgtg tgtctatcca acagggagcc acagtattta1560
aattgaccaa cctaatgtca caactacttt gaggtggcca tgttaaac aaagattt1620
atttaaagtgg tgcaattttg tataacttag catcagtagt tcaataaatt tggattgcca1680
tgcaagggct tgcattataa aaaaaaacaa aaaaaaaaaa aa 1722

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(2) INFORMATION ON SEQ ID NO. 2:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1187 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

cggtctgagg aggcgggttt ttgtgcacc caactggggc ctggaccccc tctcagcaat 60
ggccaccggc cggtctgcaca cgaactcccc ctgggggggg actccccagc aggactaccc 120
cgaccctggg tcttgaggaa gtgtgagca gcaggggact tcaccctgcc ctgccgcttc 180
ctcccggctt ccattccccac ccggggccca attacccttc ctctctgccc gatcagatgc 240
agccgcgaagt cccgcccgtc cattaccaag agctcatgcc acccggttcc tgcattgccag 300
aggagcccaa gccaaagagg ggaagacgat cgtggccccc gaaaaggacc gccaccacca 360
cttgtgatta cgcgggctgc gccaaaacct accaaaagag ttcccatctc aaggcacacc 420

tgcgaaccca cacaggtgag aaaccttacc actgtgactg ggacggctgt ggatggaaat 480
tcgcccgcctc agatgaactg accaggcact accgtaaaac cacggggcac cgcccgttcc 540
agtgccaaaa atgogaccga gcattttcca ggtcggacca cctcgcccta cacatgaaga 600
ggcattttta aatccccagc agtggatag accacactg ccagaagaga attcagatatt 660
ttttactttt cacactgtct tcccgatgag ggaaggagcc cagccagaaa gcactacaat 720
catggtcagg ttcccactgc agtcatcttg tgagtggata atcaggaaaa atgaggaaatc 780
caaaagacaa aaatcaaaag acagatgggg tctgtgactg gatcttctat cattccaatt 840
ctaaatccga cttgaatatt cctggactta caaaatgcca agggggtgac tggaaagttgt 900
ggatatcagg gtataaatta tatccgtgag ttgggggagg gaagaccaga attcccttga 960
attgtgattt gatgcaatat aagcataaaa gatcaccttg tattctcttt accttctaaa1020
agccattatt atgatgttag aagaagagga agaaattcag gtacagaaaa ccatgtttaa1080
atagcctaatt gatggtgttt gtgagcttgg tcctaaaggt cccaacaagg gagccaaaagg1140
tttaactgc tgatccctg gccaggggaa atctgtgttt ttttccg 1187

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(2) INFORMATION ON SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1478 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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gcgaacccgc gcgctgcccgc gtccctgcgct gccacagcggg aggggctgga ccccgcggtc 60
ctccctccctg ccgggtcccca tccttaaaagc gagagtctgg acgccccgcc tgtggggagag 120
agcgccgggga tccggacggg gagcaaccgg gccagggccgt gccggctgag gaggtctctga 180
ggctacagag ctgcggccggc tggcacacga gcgcctcgcc actaacccag tgttccgggg 240
ggctgtgaggg ggagggggccc gggcgccatt gctggcggtg ggagcgccgc ccggtctcag 300
cccgcctcgc gctgctctcc tcctccggct gggagggggcc gtgctcggg gccgtcgcca 360
gcccgccggcc gggtctcgaga atcaagggcc tcggcccgcc tcccgagct cagtccatcg 420
cccttgcggg gcagcccgggc gagagaccat gtttgacaag acgcgcgctgc cgtacgtggc 480
cctcgatgtg ctctgcgtgt tgcctggctgg attgcctttt gcaattctta ttcaaggca 540
taccoccttc caacgaggag tattctgtaa tgatgagtcc atcaagtacc cttacaaga 600
agacaccata ccttatgcgt tattaggtgg aataatcatt ccattcagta ttatcgttat 660
tattcttggg gaaacccctg ctggttactg taaccttttg cactcaaat cctttatcag 720
gaataactac atagccacta ttacaaaagc cattggaacc tttttatttg gtgcagctgc 780
tagtcagtc ccgactgaca ttgccaaagta ttcaataggc agactgcggc ctcaactctt 840
ggatgtttgt gatccagatt ggtcaaaaat caactgcagc gatggttaca ttgaatacta 900
catatgtcga gggaatgcag aaagagttaa ggaaggcagg ttgtccttct attcaggcca 960
ctcttcgttt tccatgtact gcattgctgt tgtggcactt tatcttcaag ccaggatgaal1020
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actctgtggc cttctcgag tttctgatta taaacaccac tggagcgatg tgttgactgg1140
actcattcgg ggagctctgg ttgcaatatt agttgctgta tatgtatcgg attttctcaal200
agaaaagaact tcttttaaaag aaagaaaaga ggaggactct catacaactc tgcattgaac1260
accaacaact gggaatcact atccgagcaa tcaccagcct tgaaggcgag cagggtgccc1320
aggtgaagct ggctgttttt ctaaaaggaaa atgatttgcca caaggcaaga gggatgcatc1380
tttctcccg ggtgtacaag cctttttaa gaccttctgc tggctgcgat gccctctgg1440
atgcacagtt gtgtgtaaca gagttaacct aactcgtg 1478

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(2) INFORMATION ON SEQ ID NO. 4:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 411 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

gccacatttc cgggggttttg cgggccccgc gatgttttcc agagcttttc aagtgggaag 60
aggagagcga caacgtgaaa atgccccgtg cgggggcgtc caccggagtc ctgccagctg120
tccggcgctg ggggtggacgt ctgatttatg aagctcccca tccacctatc tgagtacctg180
acttctcagc actgacacct acagcatcag gtacacagct tctcctagca tgacttcgat240
ctgatcagca aacaagaaaa tttgtctccc gtagttctgg ggctgtgtca ccacctacaa300
ccacagagct gtcatggctg ccatctctac ttccatccct gtaattttcac agccccagtt360
cacagccatg aatgaaccac agtgcttcta caacgagtcc attgccttct t      411

```

(2) INFORMATION ON SEQ ID NO. 6:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3181 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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cggggtggggg  ggggacaggg  ggggacagtg  ccccggggaa  cgggtgggtc  acacacacgc  60
actgcgccccg  ttagtagtgg  acattgtaat  ccagtcgggt  tgttctttgc  gcattccgcg  120
tcccttccctc  ccattagcac  gctccaaacc  ccaggttagc  catggccggg  taagacaaag  180
gccatttaga  ttagggaagg  tttaagatc  cgcaatgtgg  agcagcagcc  actgcacagg  240
aggaggtgac  aaacccattc  caacagcaac  acagccacta  aaacacaaaa  agggggattg  300
ggcgggaagt  gagagccagc  agcaaaaaac  acattttgca  actgtgtgtg  gttgattctat  360
tggctgatct  atgcttttca  actagaaaaa  totaatgatt  ggcaagtca  gtgtgtttca  420
gttccagagt  agrttttttc  tgtctgtgtt  aaatggaaac  agactcatat  cacactttca  480
attaaggtca  agccccagaa  gtgataagtg  caggggaggaa  aagtgcgaag  cacttatgtca  540
atagtgcacg  caaaggggac  agggggagag  cattgccttc  tctgccacaa  gtct  600
gtgattgttc  ttgaattctg  atcagccagt  ctcagatgcc  ccaaagtctc  ggtttcctatg  660
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atgttttttc  cttttccac  ttttaaaaga  acaatgacaa  acacccactt  atttttccag  960
gttttaaaac  agtctacatt  gagcatttga  aaggcgtgct  agaacaagg  cctctgatcc  1020
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tcccttgtag  ttgagtgtgt  tggctttctc  tctgtgaagg  tccgtgtgtg  cctgagaacc  1140
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tcaatcgtaaa  gtgctgggga  ccttaagtga  ttgtcctgt  atttttgat  attaaaaaat  1860
gtgtatata  attagctaat  tagaaaatatt  ctacttctct  gttgtcaaac  tgaiaattcag  1920
agcaagttcc  tgaagtgcgt  gatctgggtc  ttagttctgt  ttgattcaat  caagagttcal  1980
gtgctcatac  gtatctgctc  attttgacaa  agtgcctcat  gcaaccgggc  cctctctctg  2040
cgccagagtc  cttagtgagg  ggggttaact  ggaacattag  tagttaccac  agaatacagg  2100
agagcagggt  actgtgtcgt  gcagctctct  aaatgggaat  tctcaggtag  aagacaaacag  2160
cttcagaaaa  agctcaaaa  aaattgaaaa  tgtgaatcgc  agctgtgggt  ttaccaccgg  2220
tctgtctcag  agtcccgacc  ccttgagtg  cattagttac  ttatttgaag  gttttagacc  2280
catagcagct  ttgtctctgt  cacatcagca  atttcagaac  caaaaggagg  gctctctgta  2340
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atgtgcagac  tgattggcct  ggtcattggg  ctccgagaga  ggagggttgc  ctgtgatttc  2460
ctaattatcg  ctagggccaa  ggtgggattt  gaaaagcttt  acaataatca  ttctggatag  2520
agtccctggg  ggtccctggc  agaactcagt  taaatctttg  aagaataatt  gtatgtatct  2580
tagaagatga  catggggagg  gaggattcca  aaaaactttt  atttttaaaa  tatcctgtgt  2640
aaacacttgc  tctgtgtacc  tgtgggttag  catcaagttc  tccccagggt  aagatccaat  2700
cagagctcca  gtttgcatct  ggaatgtgaa  attacagtaa  tccactttcc  caaacctaaa  2760
atctgttttt  ctgcacagac  tctgagtaac  ttgtgtctgt  gtrcaatact  catagatgca  2820
ggaggtcagc  gtgatctgtt  tgaggagagc  accctaggca  gctcggagg  caataacata  2880
tggccgttct  gacctgttgc  cagcagatgc  acaggacatg  gatgaattc  cgttttctct  2940
tagtttcttc  ctgtagtact  cctcttttag  atcctaagtc  tcttcaaaaa  gctttgaata  3000

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ctgtgaaat  gttttacatt  ccatttcatt  tgtgtgtgtt  ttttaactgc  attttaccag  3060
atgtttttag  gttatogett  atgttaatag  taattccocg  acgtgttcat  tttattttca  3120
tgcttttcca  gccattgtac  aatattcaat  tgactaaaaa  caactcaatta  atcaataaaa  3180

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(2) INFORMATION ON SEQ ID NO. 7:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1964 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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gcâacatgtc  tggccaccaac  attggcattc  ctccacacgca  gagattgcâa  gggcâaatgc  60
cagtgaaggg  gcacattttcc  atccgctcca  agtctcgcgcc  actgccctct  gcggctgctc  120
accagcagca  gctgtatggc  cgtagcccat  cggcagtgctc  catgcaggtc  ggccctcgcg  180
cactggctgt  tcagcgtggc  atgaacatgg  gggttâatct  gatgcctact  cccgcctata  240
atgtcaattc  catgaatât  aacaccttga  atgccatgaa  cagctatcga  atgacacagc  300
ccatgatgaa  cagcagttac  catagtaacc  ctgcctacat  gaaccagaca  gcacagtatc  360
ctatgcagat  gcagatggga  atgatgggga  gccaggccta  tacccagcag  cctatgcagc  420
ctaaccctca  tggggaacat  atgtacacag  gccctcccca  tcacagctac  atgaacgctg  480
ctggcgctgc  caagcagtca  ctcaacggac  cttacatgag  aagatgagca  agatgaactt  540
gcaatcââââ  acttâââât  atââââââ  aggaaccttt  tatactgaca  aaccagagaa  600
âââtggaact  ttttccagtt  ââââââââ  tgtagattta  gaggaatttt  tctttgggtt  660
attttatttt  ttââââââ  tgatcttctc  tttttttggg  ttcattttgt  tctgggtttt  720
ggttttcttc  âcââââââ  âcatttttââ  gtââââââ  tctââââââ  gattttggga  780
tggggââââ  tgcaââââ  cttttcâââ  ttaâââââ  ccttââââ  tttâââââ  840
âcatggacag  ââââââââ  ââââââââ  atctttâââ  taaaââââ  gtttccctc  900
actgttttga  gctcccaatg  ttgtcatttt  taaâââââ  atââââââ  aggggtâââ  960
agâccctttc  ctccââââ  ââââââââ  ttctacttct  attccagcag  gaggcââââ  1020
ggggagactc  ggaatggggâ  atggââââ  âcccaâââ  cttaââââ  taaâââââ  1080
caggââââ  ctctctcctt  tâââââââ  tccactcctc  âcââââââ  âcctcttgââ  1140
âcccttcccc  ââââââââ  ctttââââ  ggaacttââ  gâââââââ  ttgttcttgâ  1200
atcâââââ  atââââââ  tttcttcttt  tttâââââ  tccâââââ  cactcââââ  1260
câââââââ  ctgtââââ  ââââââââ  câââââââ  gâââââââ  ggttgâââ  1320
câââââââ  ctttggâââ  ââââââââ  tcaâââââ  atcâââââ  ggââââââ  1380
ctctgtgttt  tttâââââ  ggtâââââ  ccââââââ  câââââââ  âccâââââ  1440
ttgtttctâ  tatgtâââ  gâââââââ  ctgâââââ  tgatgcttga  gccctttgââ  1500
gâââââââ  ââââââââ  cccâââââ  ttgcctctta  ggttctttct  taaâââââ  1560
gtggtgâââ  gtââââââ  gtgâââââ  ââââââââ  ââââââââ  ââââââââ  1620
ttttââââ  gâââââââ  cgcâââââ  tgtcââââ  gagâââââ  tgtgââââ  1680

gtââââââ  ââââââââ  tâââââââ  ttttââââ  cttttgââ  cctgââââ  1740
tccctgtga  atcâââââ  ââââââââ  ctctgtgâ  tggctâââ  gâââââââ  1800
ââââââââ  câââââââ  ââââââââ  tggâââââ  ââââââââ  câââââââ  1860
tgtttgtc  ccaâââââ  tctctttct  ctctgâââ  câââââââ  ââââââââ  1920
tattââââ  tcââââââ  ggtââââââ  ââââââââ  ââââ  1964

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(2) INFORMATION ON SEQ ID NO. 8:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1702 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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ggacacccca ggtatgtgga cgagcagttc ctgtcaccgc tttctctatt tgtggccctg 60
gtgatcatgt tctggctcct gattgcctaa tgctgggctc ctgcgtacat ccgtggcagg 120
gctctggact ggtgacgtgc caccocaaact cctgggtgtt ggcttccctg ctaactctga 180
ctcctggaat cagtgggata agtaacacat caaggagtct tgtttcttca tcagagcttt 240
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cagttctgca ggtcctgact ctgcagaggg aagaggcaga aagagagaaa ctgtcagagt 420
ataatttcac ctgagtttaa tattacagaa acaaaaggat gcaccaaagt gtaattcttg 480
aaattttcat gtctttaaat accccttggt aagttgcttc tgaagccagt gggggctctc 540
cagatagaga ggttcccccct tcaaatccca gtgccgtctc gttctcttcc ctccccctcc 600
cactcccccct ctctctctcc tgtagagatg caagaaattg ctgtcccata aaaatcataa 660
ttgcagtagc taaaagctggg gtcacttctg gaattccaca gagactcaaa gatcttttat 720
tggctctggg ctgtgctcag tgcctttggc ctccagagaa aacttgaagt acctctgggt 780
ttctctggca aaattattcc tgggtgagaca tgtggcttaa ctccacaggt tcccatcagc 840
ttctctccca aaactatgtt catctgcctc tctctgccag agaacataga gccgagaata 900
ctgcgcgaag tgagactgac tactgtgcat taggaaagac ctggagtcag gactttggtg 960
ggatttgtag ctccgaggca gtaataactg aacaagcagc cctgtccccc aggtctcgag 1020
agcttgtaag catcctctcc cagaacctgc cacaggaaac tgggggcttt gtcaggtcag 1080
cccactcgca tgcaaaagac caccatctcc agaagccaa gttgtcttta tgaagaggca 1140
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aactccttgt atgtgtgcta aaaccaggga agcatgtgac tgcacagcag gcaacccctg 1260
atgatttgta aagccaggtg gcaggggcctt gggggagccc agcacaaatg tattgtgtgg 1320
ttctccctcc tgtggaatgg aggggaaatt attctccca ataccttgat ttgattttcal 1380
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1702

(2) INFORMATION ON SEQ ID NO. 9:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2067 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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gcccagagct ccgcgtgttc ccatttcgag agggagctcct ggctgctatt gcaaatcacc 60
aagtctctcat cattgaaggc gagacagggt cagggaagac caccagatgc ccgcagtatc 120
tcctttgagga gggttataca aacaagggtat tgaagattgc ctgcacccaa ccccgagagc 180
tggtctccat gagtgtggcc gcccgagtg ccggggagat ggggtgtgaag cttgggaatg 240
agggttgcta cagcatccgc tttaggaact gcacatcaga gcgaactgtc ctccgtatca 300
tgacagatgg gatgtcttc cgggagttcc tctctgagcc tgacctggcg agttacagcg 360
tggtgatggt ggaatgagca cacgaaggga cctacacac agacattctc ttggattga 420
tcaagatgtg tgcctcgttc cgacctgagc tcaaggctct ggtggcttca gccacaatgg 480
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gggttctcgt ggacatcttc tacaccaagg ctccagaggg tgactacttg gaagctttgt 600
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caggacagga ggagattgag gctgcctgtg agatgtccca ggatcgctgc cgccgctgtg 720
gtcccaaaaat ccgggagctc ctgggtgctgc ccatttatgc caatctgccc tctgacatgc 780
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gctctatcac cgctctggcc tatcagcacg agcttgagga aaccacagct cctgagatcc 1080
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tgtatgctct gggagccctc aaccaccttg gggagctcac caoctctggc cgaaagatgg 1260
cagagatgcc gttggacccc atgtgttcca aaatgatctt agctctgag aagtacagct 1320
gttcagagga gatcctgaca gtggctgcca tgctctctgt caacaaactcc atcttctacc 1380
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cacgagaaga gctaggggtaa gagaaggacg taaacagaa ctagacacga ctctttttcc 1980
ttctatcatc tatttaaatc ctattaaata aaattatttt tggaataaag cttgtgggaa 2040
cattttggat ctagaaaaaa aaaaaaa

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2067

(2) INFORMATION ON SEQ ID NO. 12:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2548 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

gcccgcagccc  tcatctgccca  cccgagctctg  gttggagctg  ttgtcttcta  tgctcagoga  60
ggcccgaggaga  gaccocgggag  agagctaggc  agagtccacc  gcccgagctct  gctgcccag  120
cccgcggttac  gcacaaaacc  gccgatcccc  ggcctggggg  gagcagagcg  accaccggcc  180
gggagcagcg  cggcgagacg  cccggtgcgc  cctatgcccc  cgcgccccca  ccgcccccg  240
cgcgcgagcc  gaagcgacg  gagagaacgc  gccaccggcg  ggcccggggt  cagctagoga  300
ccctctcgcc  acctgcgcgc  agcccgaggt  gagcagtgag  cggcgagcgg  gagggcagcg  360
aggcggttcg  gggcccccct  ctgctgcggc  ggcccgggcc  tcattggcgc  catccgcaag  420
aagctgggtg  tggctggcgga  cggcgcggtg  ggcaagacgt  gcctgctgat  cgtgttcagt  480
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gaggtggagc  gcaagcaggt  ggagtgggcg  ctgtgggaca  cggcgggcca  ggaggactac  600
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tgtcccaatg  tgcccatcat  cctggtggcc  aacaaaaaag  acctgcgcag  gacgagcatg  780
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tgccggtg  catccaaacc  tacgaactac  toagtgctc  tgccaagacc  aaggaaggcg  900
tgccgaggt  cttoagacg  gccacgcgc  ccgcgtgca  gaagcgctac  ggctccca  960
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cacaggcccg  ggctccccac  tgagtgcaca  ggggtccctg  agcatgcttt  tctgaagag  1260
cggcgctcag  agtgtgtggc  tgtgtgtct  ttgactccc  ctgcggccat  ttaccaccc  1320
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tgttccgct  tcaccagcg  gacttgata  tccctgtct  gtaacataga  ccccggtac  1440
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ggctggggcca gactcccgcc caagcatgaa caggacttga ccatctttcc aaccctggg1620
gaagacattt gcaactgact tggggaggac acagcttcag cacagcctct cctgcggggcc1680
agcccgctgc gaacccctcca ccagctaccg gagggaggag ggaggatgcg ctgtgggggtt1740
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gagggaaaag aaacccacta aattttgctt tgtttccttg aagaatgtgg caacactgtt2040
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ggggcctatt tttttttttt tccacaaggc attctctaaa gctatgtgaa attttctctg2160
cacctctgta cagagaatac acctgcccct gtatatcctt ttttccccc cctccctcc2220
cagtggtact tctactaaat tgttgctctg ttttttattt tttaaataaa ctgacaaatg2280
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atagtctgta aaaatccct tgtgaattg gaacaaggga gatattctcc taggcgagat2460
cctttcttgc caactccgtt tcccttatag caaatgtagt aaatgaggat gaagtcctct2520
tgagagcatg tgggggttgg gtgaccaa                2548

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(2) INFORMATION ON SEQ ID NO. 13:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1673 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

| | | | | | | |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| accaatgac | atgtagtaat | caaatgtttg | gggctagata | ttatggtata | caaaaaacat | 60 |
| taaaatcatg | tggtttgcaa | gcaaaagcaa | catttttgcc | aatgtttgca | aattggccac | 120 |
| aaccacaaat | tcaagaaact | ttttaaaaag | acaaaagcca | gcttacaaga | atttgaccaa | 180 |
| taaaacccct | cgagccca | gccttatcag | ctgggggtga | gggaagactg | gtctaggtgc | 240 |
| tgctcctgaa | cttggtctct | gagccatggc | ttcccataga | cactcaggtc | cctccagcta | 300 |
| caaggtgggc | accatggcgg | agaagtttga | ctgccactac | tgcagggatc | cottgcaggg | 360 |
| gaagaagtat | gtgcaaaagg | atggccacca | ctgctgctg | aaatgctttg | acaagtctctg | 420 |
| tgccaaacac | tgtgtggaat | gcgcgaagcc | catcggtgog | gactcccaag | aggtgcaacta | 480 |
| taagaaccgc | ttctggcatg | acacctgctt | cogctgtgoc | aaagtgccttc | accccttggc | 540 |
| caatgagacc | tttgtggcca | aggacaacaa | gatcctgtgc | aacaagtgc | ccactcgggg | 600 |
| ggactcccc | aaagtgaagg | ggtgcttcaa | ggccattgtg | gcaggagatc | aaaacgtgga | 660 |
| gtacaagggg | accgtctggc | acaaagactg | cttcaacctgt | agtaactgca | agcaagtcat | 720 |
| cgggactgga | agcttcttcc | ctaaagggga | ggacttctac | tgcgtgactt | gccaatgagac | 780 |
| caagtttgcc | aagcatttgc | tgaagtgc | caaggccatc | acatctggag | gaatcactta | 840 |
| ccaggatcag | ccctggcatg | cogattgctt | tgtgtgtgtt | acctgctcta | agaagctggc | 900 |
| tgggcagcgt | ttcaccgctg | tggaggacca | gtattactgc | gtggattgct | acaagaactt | 960 |
| tgtggccaag | aagtgtgctg | gatgcaagaa | ccccatcact | gggtttggta | aaggtccagc | 1020 |
| tgtgttggtc | tatgaaggac | aatcctggca | cgactactgc | ttccactgca | aaaaatgctc | 1080 |
| cgtgaatctg | gccaacaagc | gctttgtttt | ccaccaggag | caagtgtatt | gtccgaactg | 1140 |
| tgccaaaaag | ctgtaaactg | acaggggctc | ctgtcctgta | aaatggcatt | tgaatctcgt | 1200 |
| tctttgtgtc | cttactttct | gccttatacc | atcaataggg | gaagagtggg | ccttcccttc | 1260 |
| tttaaagtct | tccttccgtc | ttttctccca | ttttacagta | ttactcaaat | aagggcacaci | 1320 |
| agtgatcata | ttagcattta | gcaaaaaagca | accctgcagc | aaagtgaatt | tctgtccggc | 1380 |
| tgcaatttta | aaatgaaaac | ttaggtagat | tgaactctct | gcattgtttc | catagagcag | 1440 |
| aaaagtgtca | atcattttagc | cacttagtga | tgtaaagcaag | aagcatagga | gataaaaccc | 1500 |
| ccactgagat | gcctctctatg | cctcagctgg | gacccaccgt | gtagacacac | gacatgcaag | 1560 |
| agttgcagcg | gctgctccaa | ctcactgctt | caccccggtt | ctgtggagcc | gggagaaggg | 1620 |
| accctacttg | accatggcat | ggggttaact | ttcctcatca | ggactctggc | cct | 1673 |

(2) INFORMATION ON SEQ ID NO. 14:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1593 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

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ggggccaggga cggccggcgg cgcggaagtgg ctgccctcg cggggacact cagagcccg 60
tgggcggggag gaaggcgga tgcccagac ggtgatcctc cggggccctg cgccctgggg 120
cttcaggctc tcagggggca tagacttcaa ccagcctttg gtcatcaccg ggattacacc 180
aggaagcaag cgggcactgc caacctgtgt cctggagatg tcatcctggc tattgacggc 240
tttgggacag agtccatgac tcatgtgat gcgcaggaca ggattaaagc agcagctcac 300
cagctgtgtc tcaaaattga caggggagaa actcacttat ggtctccaca agtatctgaa 360
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gagaagacat tcatggcttt gggcagaagg attgtgcaga ttgtcaactc caaatctaaal1140
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cagccatcaa acacataaac atcaagata ttgaaggact ctaattgtct ttcccttgacal1380
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agttgtctgt atgtgtttta actattacag tgcattgttag ggagaaattc cctgaatttc1500
tttagttttg tattcaaaaca attatgccac tgcattgcaac aaacataata aatacataaal1560
agatttaaaa aataaaaaaa aaaaaaaaaa aaa
1593

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(2) INFORMATION ON SEQ ID NO. 17:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1722 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

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cattgttttcg caaaatccca ggcagcatgg acctcagttc tctctgggta cttctgcccc 60
tagtcacccat ggcctggggc cagtatggcg attatggata cccataccag cagtatcatg 120
actacacgga tgatgggtgg gtgaatttga accggcaagg cttcagctac cagtgtcccc 180
aggggagcgt gatagtggcc gtgaggagca tcttcagcaa gaaggaaagt tctgacagac 240
aatggaaacta cgcctgcgat cccacaccac agagcctcgg ggaacccacg gagtgtcgtg 300
gggaggagat caacagggct ggcattgaaat ggtaccagac gtgctccaac aatgggctgg 360
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gttgctcgcta cagcaagagg tgcccataat cctgctggct aacaacagaa tatccaggctc 480
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gaagtttctg ctgctctctt tcttctctcc tgagctggta actgcaatgc caacttctctg 780
ggcctttctg actagatata cacttctaat aaaatccaca attaaacctat gttttctcatc 840
tttcacatgt ttcatagcaa ctgctttata tgactgatga tggcttccct gcacaccaca 900
tatacagttg ccatgcttac agcggggctt ctggagcacc agctgcagcc tggctactgc 960
tttttactgc agaatgaact gcaagtccag catagtggag gggagaggca gaactggagg 1020
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aaattagaaga caaacggttag cataccagat aaggaaaaat agtgccaggg ccaggggaaac 1320
ccgtgaggat cacttccaaa tgagattaaa aacaaggaa gtacagagatg 1380
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gggaaaggct gcctggggga tcaactttcc ttctgtgtgt ggctcagga tctctctgca 1620
gagatggcgc tatctttctc cctcctgtga tgtctgtctc caaccattt gtactcttca 1680
ttacaaaaa aataaaaaa ttaacgttca ctatgctgaa aa 1722

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(2) INFORMATION ON SEQ ID NO. 18:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1648 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

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tgaccaagaa acagggccta aggatcattt tctcggatgc atcacggctc atcttcocggc 60
tcagttcctc cagtggtgtg cggggccaccc tgcagactgt acgcagagag ctacgagagg 120
gatccacagc gccatgacca ggagccacag gcagtgctga gccctctcat agccatcgca 180
ctgaaaaaat cccagattca tgagagaact ggccggaggg gaccocactgt catcacctga 240
atagaggaaa gatcactcac caggggccaaa gagagtgtct agcggggagat gcttcactga 300
tgccttcttg ctacctgttt gtgcctctta tgactttgga aaaacaaaaa atattttgtct 360
tttgggggat agaggggtgg tgggaaaaga aaaaaaatcc atttggtttt gggtttgtcc 420
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tctacatttt atcacacaaa ggaacctccc cttttgacaa caactgggct aggcagctgt 540
taatcacaca atttgtgat cacttgtgcc aagttagaaa atgttctaaa atcacagag 600
agaacagtg cagaatgaaa ctgaccttaa gtcccagggt cccctgggca ggcagaagga 660
gacactcccc gcatggagga gggtttatct ttctatctta ggtcaggtct acaatggggg 720
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gcacagtcac taacctctgc atttgcggaa atgacctggg gcactttgac tgttaagcaal 1500
tgcgttattg ctgtagtcaa gttttagtga agcaaggaaa catctccagt aaggtatttg 1560
ttcccaattt ctgtctgtgc ttctgtcaga aacttgcctg gacttttagt gcccaataaaal 1620

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aagaaatccc taatttcaac cttaaaaa

1648

(2) INFORMATION ON SEQ ID NO. 20:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1610 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

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gcgcgctgat  tggacgcgtg  gggcgaggcg  gaggagagcc  gtgcgcacgg  cgtatgtggg  60
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tgcgagccgt  cttcccccagg  cctgcgtccg  agtctccgcc  gctgcggggc  cgctccgacg  180
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gccacattgc  caaggactgc  aaggagccca  agagagagcg  agagcaatgc  tgctacaact  480
gtggcaaac  aggccatctg  gctcgtgact  gcgaccatgc  agatgagcag  aaatgctatt  540
cttgtggaga  attcgggacac  attcaaaaag  actgcaccaa  agtgaagtgc  tataggtgtg  600
gtgaaactgg  tcatgtgacc  atcaactgca  gcaagacaag  tgaagtcaac  tgttacccgt  660
gtggcgagtc  agggcacctt  gcacgggaat  gcacaattga  ggctacagcc  taattatttt  720
cctttgtcgc  cctctctttt  tctgattgat  ggttgatata  tttctctga  atcctcttca  780
ctggccaaag  gttggcaga  agaggcgaat  cccagggccg  tgagctttac  ttgcccgtga  840
aaaggaggaa  aggggtggaa  aaaaaccgac  tttctgcatt  taactacaaa  aaaagtttat  900
gtttagtttg  gttagaggtg  tatgtataat  gctttgttaa  agaaccocct  ttccgtgcca  960
ctggtgaata  gggattgatg  aatgggaaga  gttgagtcag  accagtaagc  ccgtccctggg  1020
ttccttgaac  atgttcccat  gtaggaggtg  aaaccaattc  tggaaagtgc  tatgaacttc  1080
cataaataac  ttttaatttt  gtataatgat  ggtcttggat  tgtctgacct  cagtagctat  1140
taaataacat  caagtaacat  ctgtatcagg  cctacatag  aacatacagt  tgagtgaggag  1200
taaacaaaaa  gataaacatg  cgtgttaatg  gctgttcgag  agaaatcgga  ataaaagcct  1260
aaacaggaaac  aacttcacat  cagtgttgat  gttggacaca  tagatggtga  tggcaaaggt  1320
ttagaacata  ttaattttcaa  agactaaatc  taaaaccocag  agtaaacatc  aatgctcagag  1380
gttagcatata  tttggagcca  ttccaggaat  gcagagaaat  gcattttcac  agaaatcaag  1440
atgttatttt  tttatactat  atcaacttag  caactgtgtt  tcatttgtgt  taatcagttt  1500
ttaaaagtca  gctggaaaga  gcaactgaag  tctagaaaaa  tagaaaagta  attttaaacat  1560
attccaataa  agctggaggga  ggaaggggaa  aaaaaaaaaa  aaaaaaaaaa  1610

```

(2) INFORMATION ON SEQ ID NO. 21:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

ggaggcgccg ggagagtagg gtgctgtggt ctgagctaga ggggtgaagct ggcggacagg 60
aggatggcg tatgcaggtg atagactaga gaacaagacc tctgtctccg tagcatcctg 120
ggcgagcagt ctgaatgccca gaatggataa ccgttttgcg acagcatttg taattgcttg 180
tgtgtcttagc ctcattttcca ccatctacat ggcagcctcc attggcacag acttctggta 240
tgaatatcga agtcaccgttc aagaaaattc cagtgtattg aataaaagca tctgggatga 300
attcatttagt gatgaggcag atgaaaagac ttataatgat gcacttttcc gatacaatgg 360
cacagtggga ttgtggagac ggtgtatcac cataccctaa aacatgcatt ggtagagccc 420
acgagaaaag acagagtcac ttgatgtggt cacaaaatgt gtgagtttca cactaaactga 480
gcagttcacg gagaaatttg ttgatcccg aaaccacaat agcgggattg atctccttag 540
gacctatctt tggcgacttt agttcctttt acctttttgt agtttaggtt tgatgtgctt 600
tggggccttg atcggaacttt gtgcttgcat ttgccaagc ttatatccca ccattggccac 660
gggcattctc catctccttg cagggtctgtg tacactgggc tcagtaagtt gttatgttgc 720
tggaattgaa ctactccacc agaaactaga gctccctgac aatgtatccg gtgaatttgg 780
atggtccttc tgccctgctt gtgtctctgc tcccttacag ttcatggctt ctgctctctt 840
catctgggct gctcacacca accggaaaaga gtacacctta atgaaggcat atcggtgggc 900
atgagcaaga aactgcctgc tttaacaattg ccaattttat ttttttaaaa taatactgat 960
attttcccca cctctcaatt gttttaattt ttaaatggg ggatatacca ttttattatg 1020
gaaaatccat ttaatttata caccatccac cactaaatac ccccttaat accccctaaa 1080
atttaagggg ggttacctta aagcgatg

```

(2) INFORMATION ON SEQ ID NO. 22:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 675 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

agggaaagag agagagagagc ctagacgaac acaatcacat gttttctttg ctgttcctcc 60
cgggatgggc ctgttttggg gtttgggact ctgaaccoga gcgggggttc ttcgcttgac120
tttgatcctg gtccctaaat gcctttcccc actccccctc cgtgggttca ggggccaaag180
ggccccctcc cagagcacgg gcagcacctg ctctggacc cctgtgtgcc agcctctgca240
gacgcagctg gtgggagggg gcatggattt ggagggtggag aagtcactcc tggctcctgg300
aggggggtgg ctgtgtgctt agttcagtg gactcgggga ttggtgaggg cggacagggt360
tctgagggct ccctagcctt ctttgtaaat tcacacgaga tagtccaggg ctttccagcg420
cccagcttgg atgataatcc tegtgtcccc cactctaagg cctccttgag attttlttgg480
ggtctaccac gtccctctgcc tgtctccagg tggtagagga gatgtggttc ctgtccctct540
cctgggtccc tagggggccc caggggccct ccctgtagct ttagctgacc ccattggtgt600
gggtgtgggg tctgtgcgcg tgctcaggta agcttggggg ctccaggtaa gcggtcccga660
agaacggggg gggag

```

675

(2) INFORMATION ON SEQ ID NO. 23:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 350 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

agcagagcaca ggttgggttc gctcctcttg cagaaacctg gctctcagga ggtccttgtt 60
ccaggggaaca gctgcttctc tgggggcttg ggcttctaac ttccctggca gccctctggc120
actaaccacag ctggaacaac ggggaacaaa cggcctggag tgccaaaccc ttctgtctat180
ttttttccag aaaaacgggg gcaatggctg ttgaggagcc catttgggaa gaactggtgc240

ctctaatggg gcaaatggat tctgcagggg gctgcagttg ggcagggaaa attccttcaa300
acaagggggt ccaccccaaac ccaggccccg gcttcaaatg gccagaaaaa 350

```

(2) INFORMATION ON SEQ ID NO. 24:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 746 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

ccccccctcc tccggtttt ttttttttat ttaagaaat ttattttctac ttctacagca 60
gaaatacggg aatggtacag gtttgggcaa atcatacttt atgaaatgga ttctcatacc120
acâtcctttt taatacaggc acgttataac ataattcctg gattttcaaa atccagccaa180
cacggatacc tctgctactc tgttttggcc ttcatactg cttcctcttt cagacgagct240
ttctttttct agttcaagct tgttaaagtc tctgtgtctt gggcagcctt cttgccctca300
ataaccatga agatgcaccc taccaccgtc agggcaatca ttagatagct gatcttcaact360
cgcactctgt tctttgcagc atcaagcctc tccaaagaga cagtctctgg gatttcatct420
tcctttttga agcgacctga ccatacgagg atctttttct gccaatccgt aggtttgtgt480
aaaggcactc tgttgttaagt gggggatgga gctccgggac ttctctgtgg ttttgtgcaa540
aatccattta ttctcttcaa atcagagctt ctggtaagcc ttagagatga gaaaacatct600
ctttcacata acctaaaaa cgttctctgt gccaggcgca gaccgctgag gctcccatg660
gccacttgct actccgccga ccagcgca ga acttcgccgg ggacggtggc gctggtgagc720
tcaatgtcac ccagcgcttg agtggg 746

```

(2) INFORMATION ON SEQ ID NO. 25:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 217 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

agtgtatggc agcaaatgag ggatcataac tctcagttta ttgatgatta ttcactctca 60
gatggaggag ttatcccgtc agccacttca gtttgccttt aaaacaggag cccacaggac120
ccaagggaact attaaggagg accaggaacc taggtttttt ctttcaaaaa attggccctal180
gcccaataaa tgaaggaaaa aattaggcac ctttttt 217

```

(2) INFORMATION ON SEQ ID NO. 26:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 392 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

gcgggacccgg cggtctccac tgatcttttc caaggctgta cagacatggc ggcggctttt 60
cggaaggcgg ctaagtcocg gcagcgggaa cacagagagc gaagcagtga ctacgtaaa120
aaacaagaat acctcaaagc tcttcgggaag aaggctcttg aaaaaaatcc agatgaattc180
tactacaaaa tgactcgggt taaactccag ggtggagtac atattattaa ggagactaag240
gaagaagtaa ccccaagaaca actaaagctg atgagaactt caggacgtca aatatatagg300
aagggaagag ggtgcagaag ctaagaaaaat cgaagactaa aatcagggcc catctgcggg360
ttgcagggga ggcaggaaaa ggttggtttt tt                               392

```

(2) INFORMATION ON SEQ ID NO. 27:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1796 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

cggctcgaac gtattagtgt ttcttaattt ttttccagc aaaaatgga tcttttaaga 60
agaatttgag aagcaaaaca ttacatgtca tgtcaagggt gtagcagatt ccatttggct 120
tcaatattgc cacaataccc agggattaat gctgccacag gggggcaact tttatttgtc 180
ttacttccta ccccttccct gtctcgcttc ttaactcag ttaagtgtgt ctgtttggga 240
cctggaaaag aaccocaaaga aaacctgagt ggacagggtc atttctggaa tgcagaaaaa 300
attttaaagg ctatgatttt agaatactct caactagcat tctttccatt gatttgaagg 360
ggaaattaac tattataatc tcttgaatcc aaaactggat attaagaact ttccccctta 420
ctaagtgtta gacttttgtc atgtggtgag tcaataaaga ccattttgat tgtaaaacct 480
aaaatagttc agcaagttag ccacagtctc ggctaacag cagacttgcg gttttcactt 540
ggatatcctg agttgggttg ctaaccttaa tttctatgat gttttctaaa atgaaacttg 600
ataaagtaga ccaccagctg caccgtgttt tctgtaaaag tattgttagt aagtggccaa 660
gagacttgag gaaaaatacag attttttgtt taccttggct ttgttttaag tcttaaaaaa 720
taaagataaa cattataatg tagaatacag atgggacata gtccctgtaa gcttcccttg 780
aaaaatgtttt aaattatttg gaagctttta aaagacacta aattgtactc taaaagacac 840
taaatgttac taattgtaca aaggtcaagc caattttatg aaacagtcct acagagtaat 900
atatgtgatg cagtgttaaga aggaaaaata tcatctctaa cattatggta ataacattta 960
gctccttagg agttggagca gggggatggg taattacaga ttgacagact atagaaaagag 1020
tttcattttt ttgtgacccc acagagtctc aaatttttat ttccactacc gctagagcct 1080
actgtgaaat cactgtccca tatttgccag tggaggaaat gggcatagag tagagaaatag 1140
cttcatatgt ttacacgttt gcatagacta cacacatgtc atgcgtttat ggcaggttagc 1200
tggattttat tccccaaagt aataatgttg aagtatgggt ctcatcattc ccatacacag 1260
aaacacaaaa cactttgatc ataaactttt ttcttcagaa gccaaactaa cttgcagaat 1320
aatagagcca ctggtttaat gtttctcaca gatagggttt agtgaagct agtattctgt 1380
gtgttcgtag aaatgattca atacctgcag ctgggtgaatt aggaattgta ttgttgcc 1440
tttttatatt agatgaggtg caaaaaattt aatgctagtc agtatgcacc accacagga 1500
agttagatcc cattagcact tgaaactaca gctttggaaa cttaggctaa gtttaatttg 1560
atttgttact tgattccact actgaccttt tcttttgttt gaagtgccta tcagcataat 1620
gagctaaagt tcatgcatat ttgtgaagaa acaccctttt tggtcocctt tgggacagag 1680
aggtaactct tgatctttat gaatgacagg ttactgtttt gccttattgc ttaactaat 1740
gtagtgaat aaagcagaca aagcttgaaa aaaaaaaaaa aaaaaaaaaa tcgacg 1796

```

(2) INFORMATION ON SEQ ID NO. 29:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2927 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| gaagaaaaag | aggagaaaa | aggtaggagg | aaataaagg | aggagagaag | cacagtgaag | 60 |
| gaaaaaaaaa | gtcccttttc | gacatcacat | tcctgtgrrt | tcctccagcc | tggaataaat | 120 |
| attaatccca | gtccttttac | gcccggaaac | aaagagacta | agccagacta | tgggggaaaag | 180 |
| ggagataaga | aggatccctg | aacttttaag | agggaagag | tgagatttcag | aaatccgccag | 240 |
| gactggactt | taagggaagt | cctgtgtcag | cacaaggagc | tgccacacac | agcacacaga | 300 |
| gaccaggagc | aaactgcaga | caaatggaga | tacaaagact | tagaaggaga | gtccctttca | 360 |
| ccctcatccta | ctgtgtccaga | aggtaaaaag | acacagccag | aaagaaaagt | catcggtctca | 420 |
| gtcttcagat | caggacaggc | tgtggatctg | gtgcgggtact | ctgaagactg | ctctgcagcg | 480 |
| acaccctttt | tgtattgttc | acccctggta | aagagagaga | gggctggggag | gaaaagttagt | 540 |
| tcactctagga | aactgtccctg | ggaacccaaac | ttctgatttc | ttttgcaacc | ctctgcatttc | 600 |
| catctctatg | agccaccatt | ggattacaca | atgacattga | gaatggggacc | ccgttttcaat | 660 |
| atgctgttgg | ccatgtgggt | agtgtgttga | tcagaacccc | accccatatg | cactatttga | 720 |
| ggcagccacg | gaggacggaa | agtgcctttg | gtttctccgg | acagcagtag | gccagctcgg | 780 |
| ttcttgaggc | acactgggag | gtctccggga | attgagagat | ccactcttga | ggaaacccaa | 840 |
| cttcagagctc | tcacagagaag | gaggagtgtg | cccgtgttga | gactagctgc | cccaacagag | 900 |
| ccgcccagccc | gtctgggacat | caatggggcc | gcccgtgagac | ctgagcaaa | accagcagcc | 960 |
| aggggctctc | cgctggagat | gatcagagat | gaggggtccct | cagctcgctc | agaaagtgtg | 1020 |
| cgtttccctt | cggtgtccag | ctctcccaac | atccttgcca | gctttgcagg | gaagaaacaga | 1080 |
| gtatgggtcca | tcacagcccc | tcagtccctc | gaaggcttact | accgcctcat | gatgagcctg | 1140 |
| atgtagggag | atgtgtactg | tgagctggcg | gagaggcaca | tcacaacagat | tgtgtctctc | 1200 |
| caccagggag | gtgaggaagg | aggcaagggt | agaaggatca | ccgcgagggc | ccagatccctg | 1260 |
| gagcagccgc | tggaccctag | ccctcatccct | aaagtgtatga | gcttctctgaa | gcttgagaag | 1320 |
| ggcaagtgtg | gcattgtgct | gtcgaagaag | acgctgcagg | tgaggaggcg | ctatccatat | 1380 |
| cccgctaggc | tggaagccat | gtacgaggtc | atcgaccaag | gccccatccg | taggatcgag | 1440 |
| aaagtacagg | agaaggcctt | tgtccagaaa | tgtaaaggct | ctgggtgtaga | gggccaaggt | 1500 |
| gtggcggagg | ggaatgacgg | tgagggggga | gcagggaagc | caagcctggg | cagcgagaag | 1560 |
| aagaaagagg | acccaaggag | agcacaagtc | ccaccaacca | gagagagtgc | ggtgaaaggt | 1620 |
| ctgagaaaaa | tggccgcacc | tgccccagct | ttgccccaac | ctccctcaac | ccccagagcc | 1680 |
| accacccttc | ctcctgcccc | agccacaaca | gtgactcggt | ccacgtcccg | ggcggttaaca | 1740 |
| gttgctgcga | gacctatgac | caccactgcc | tttccccaca | cgcagaggcc | ctggagcccc | 1800 |
| tcacctctcc | acaggcccccc | tacaaccact | gaggtgatca | ctgccaggag | accctcagtt | 1860 |
| tcagagaaat | tttaccctcc | atccccgaag | gatcagcaca | gggagaggcc | acagacaacc | 1920 |
| aggagcccca | gcaggccac | cagcttgtag | agcttcacaa | atgccctcc | caccaccatt | 1980 |
| tcagaaacca | gcacaaggcg | tgctggccca | ggcgttttcc | gggacaaccg | catggacagg | 2040 |
| cgggaaacat | gcacccgaga | cccaaatgtg | gtgccaggct | ctcccaagcc | agcaaaaggag | 2100 |
| aaacctccca | aaaaagaagg | ccaggacaaa | attcttagta | atgagtatga | ggagaagtat | 2160 |
| gacctcagcc | ggcctactgc | ctctcagctg | gaggacgagc | tgcaggtggg | gaatgttccc | 2220 |
| cttaaaaaag | caaaaggagt | taaaaagcat | gaaaagcttg | agaaaccaga | gaaggagaag | 2280 |
| aaaaaaaaga | tgaaagaatg | gaacgcagac | aagttactta | agagtgaaaa | gcaaatgaag | 2340 |
| aaagtctgag | aaaagagcaa | gcaagagaaa | gagaagagca | agaagaaaaa | aggaggtaaa | 2400 |
| acgaacagag | atggctatca | gaaacccacc | aacaaacact | tcacgcagag | tcccaagaag | 2460 |
| ctagtggccc | acctgctggg | gtcctttgaa | ggcaaacgaa | gactcctctc | gatcaactgt | 2520 |
| cccaaggctg | agaaacaatat | gtatgtgcga | caacgtgatg | aatatcttga | aagtctctgc | 2580 |
| aaagtggcta | ccaggaaaaat | ctctgtgata | accatctctg | gocctgtcaa | caacagcacc | 2640 |
| atgaaaaatg | accactttca | gctagataat | gagaagccca | tgcgagtggg | ggatgtgaa | 2700 |
| gacttggttg | acagcgttct | catcagcgag | ctgaggaaag | agtacggaat | gacctacaat | 2760 |
| gactttctca | tggtgtcta | agatgtggat | ctgagagtca | agcaatacta | tgaggtacca | 2820 |
| ataacaatga | agtcgtgtgt | tgatctgata | gatactttcc | agtcccaagt | caaatgatgt | 2880 |
| gagaaccaga | agaggggggt | tttttttgaa | gggggaaaaa | cgcccccc | | 2927 |

(2) INFORMATION ON SEQ ID NO. 30:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 743 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

tccgtggggc tttaaaaaat ggttggtgggt gtgtgggttt ttttgagggt ggagaggatg 60
tgtgaaaaatc ttttccaggg aaatgggttc gctgcagagg taaggatgtg ttcctgtatc120
gatotgcaga caccagaag gtgggtgcac actgcatgct tgggggtgcc aagggtatcg180
agacctccaa catacttgtc tgaagctcgt gcgctggcc atggccocctc tgccaagcct240
gtgtgcgatg ccccttgggtc tttagtgc aaagcctagg ctccagaagca cagcagcgcc300
atctttccgt ttcagggggt gtgatgaagg ccaaggaaaa acattttatct ttactatttt360
acctacgtat aaagttttag ttccattgggt gtgcgaatac ccccttttat cactttttaa420
tttgacattt attttttttc ttccatgctt gttctctgga catttgggga tgtgagtggt480
agagctgggt agagaggagt caggcgccct tcccaccgat ggtcctggcc tccacctgcc540
ctctcttccc tgccctgatc ccgctttcca atttgccctt cagagaactt aagtcaggga600
gagttgaaat tcacaggcca gggcacatct tttatttatt tcattatggt ggccaacaga660
acttgattgt aaataataat aaagaaatct gttatatact ttccaaaatc caaaaaaaag720
tagggagggt aagaaaaaag ggc

```

(2) INFORMATION ON SEQ ID NO. 31:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1667 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

agagccaata gcatgggggt tacaaggcaa agatagtcac tcattcaaca catattcata 60
gagctccctc tctgtgccag acactgttct ggaagatagc tagatgaaaa cctttgcact 120
cacagagctt acatgccagt gagtgaagat cgatgataaa taaagcaaat gcatacatatg 180
ttcacatttg ataagtatat gccaaaaaat gaagccggga aggaggacaa ggcccatggg 240
tgggtgttga ggtttttaaa gtgtggtcag gaaaggcccc actgataagg taacatttga 300
gcaagtctga aaaaggccaag gggatctttg gggctaactt cgggatccct gcactttatg 360
taagaatgta aacctggagt ctcatttaag aatgatcagc aatacgttta gaacatatga 420
actgaatgaa atggacattt tttcttaatt tacgtataaa tccatatgat tatacataaa 480
gttctgatgc attaataaaa gcagccaaat agggccaaag agaaaaataa caggactctg 540
tactggacct aactttatca ttaattaggt aatattttcc tcatttcttt actgctgcc 600
ttttctcac cagtattcca gagatggcca tagctcata ctctaccacc aagaacctaa 660
aaggaaattag aatacacgag aattggcctc agtgaagagc ttaaaattgt tctcctcgta 720
gaactggact attgatcatt accacgtgac gttggctcta ttactttctg ttcccaatgt 780
cctctagtgt gtttgaaaat gttaaaacat ccttaaaatc taaatcatat aatcagaatt 840
ctatagtgtc caactctatc tgaataagatc atttggaaga ctttagaact tattaaattt 900
aaaaaggaata tttattagcc atatgcagaa tttctaata tgatatgtga cagcttctaa 960
ttcacttttc agatcagtg ttgaaatggc aattatcagt gttggattta gttccaaacta 1020
cttgatttac aaaaatgtac atttagagaa ggttaaaaga aacagtgaga aatgtaaacaa 1080
ttcaaaatga taattgaatc tctcagttgt gggaaataat atcagagaca tgcactgaa 1140
aatgtctcac ctttcattct tttttcttaa ttcataaagt tatctgttag aatttgatga 1200
gacctctcta gtcatttcca actggggcgg tgcgtgcacc gaatggtgtt tgagagtgtt 1260
ggggctaggg cacatttttg gttgtcacag caactggggt ggcattttgt gccagctgcc 1320
aggaatagta acattatgaa tgccagggac agtgtgtcca gtaaagctct ccattccaaa 1380
ggggcagggc acgggtgtct acgctgttaa tccagcactt ttgggaggcc aaggtggggc 1440
gatcacctga tgtcaggggt tcgagaccag cctggccaac atgggtgaac cctgtgtcta 1500
ctaaaaatac aaaaattggc tgggtgtgtt gtcacatgcc agtaacccca gctactaggg 1560
aggctgaggc aggagaatca cttgaacccg ggaggcagag gttgcagtga gctgagattg 1620
caccactaca ctccagcctg gatgacagag tgagacttca tctcaaa 1667

```

(2) INFORMATION ON SEQ ID NO. 32:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

cgtggtaggc  acctcatcag  tgtttactga  ttgaaaacat  tgttgactgt  ggcttctatc  60
agagtgtcta  ccttttacag  ctctgacctt  acctcattta  atttgctgct  tttaatctac  120
gggggctgag  aatttgtgaa  accagtgttg  ttagaagtgt  atataatctg  aatcaataag  180
ctctgaatgg  gggacaagaa  acgctcttat  agcacaaaga  tgcattggact  tcatgacagc  240
tcttttggt

```

(2) INFORMATION ON SEQ ID NO. 33:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1246 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```

aatggaaggt taattaccgg ggcccacctt gagacggaaa aaaatttgga aaacgaaact 60
aaaaatgggt ggggtgaatt tctacccaaa gtccagcggt ggtggctgca ctggcacaga 120
atactaaact gagtgtgact attttcaatg caacaaatga aaaaacaaaa tgtgcctgtt 180
taaagcactc agtagagggc tgatgaaact aatttttttt cttttaagac atgcactctt 240
gagtctctca gtaactgagt gttgttttag acagcacaaag aagggggtgag agtgcgtctc 300
ctagccttaa tegtgggaggg tagtttcagt cactcatcgg ctttcaattt tgtgcagaaa 360

tattagaaaa cctcattgat caattttatg tatttgaata tcagcaaat gaaattttcc 420
ataattatca ttaatttgta accacatcca gtgtcatgct tactccttag agttcagatg 480
aattcttaaa attaaaaaaa aactccatag tactaatttt gtttctttat atagtttggg 540
tttgatatta gtgcttgcaa ttgtattaaa gtcaaaagct gatttttatg gcatacacaa 600
gaatgcactc ttttctttta ttccatacca ataattttaa gattgatgat ctaaaaacaa 660
tttgcaacgc actaaagcat gagctacttt catctaaacc tgtaaaaata tgaaagattt 720
ttatattttt tcaactggaa gaaattcttc ctggatgaaa ttacaaatat gtgtagaata 780
tatttaataa aagacttata aaatacctaa ctacaggact taaaaatag attggcgctg 840
agtataatga acaatattcc atataataaa gtttagcctt tataaaaaatg aagttgcagg 900
ctgacattac attctgtact tactaagtgt caacagccct tacaacacatt aaatgtaaaat 960
ggtttcaaat ggtagcgtgt gtttaaatgt aatcatgtta ttttattcat tgttaatgct1020
ttgatgaaaa ggcttttatat gcagtagatc tacgaaaata ttgttcatac tgatcagaat1080
taaatattga tagagcagag ttttaaaatg aatgtaaaata gcactaaacg ttttctttct1140
gcaacctgta cttacagatt ctctctgtaa actaaataaa aaaaaaatga tagtgcaaaa1200
aaaaaaaaaa aaaaaaaagag acggagagag gagaaagagg gcgtgg 1246

```

(2) INFORMATION ON SEQ ID NO. 34:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 215 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```

gggaagcatt ttggatatga tgcaggaaat ctcttcctgg agtcaaaagt tcccaagagg 60
tgctgtatatt ttaagaaatg gagtttatatt aaataatagt taagcttggc cccatgtgg120
ccgggcaact tttttcaatg gtgcttatta gaagaaagtgt tttcatctgg tcaatttaag180
gaaataaaa taggaaatgg agaggggggg agaga 215

```

(2) INFORMATION ON SEQ ID NO. 35:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 734 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

gctgcgcggg ggcctggggct cggcgctcggg ccccggggga tgtggagagc tggcagcatg 60
tcggcccgagc tgggagtcgg gtgcgcattg cgggcgggtga acgagcgcggt gcagcaggct120
gtggcgcgggc ggccgcgggga tctcccagcc atccagcccc ggctagtggc ggtcagcaaa180
accaaacctg cagacatggt gatcgaggcc tatggacatg ggcagcgcac ttttggcgag240
aactacgttc aggaactgct agaaaaagca toaaatccca aaattctgtc tttgtgtcct300
gagatcaaat ggcacttcct tggccacctc cagaacaaca atgtcaacaa attgatggct360
gtccccaatc tcttctatgct ggaaacagtg gattctgtga agttggcaga caaagtgaac420
agttcctggc agagaaaagg ttctcctgaa aggtttaaagg ttatggtcca gattaacacc480
agcggagaag agagttaaaca tggccttcca ccttcagaga ccatagccat cgtggagcac540
ataaacgccca agtgtcctaa cctggagttt gtggggctga tgaccatagg aagcctttggg600
catgatctta gtcaaggacc aaatccagac ttccagctgt tattgtcgct ccggaagag660
actgtggtta aaagctgaac atccctgctg aacaggttga gctgatcatg ggcatgtccg720
tctgtaaaact gcaa

```

734

(2) INFORMATION ON SEQ ID NO. 36:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

gctgctgggg agccactgaa ccaaccggag acccgctggt cccacgtgaa gcagctgtcc 60
tggtgtggag gtacagagct agaccagcac tggccctccc agccccctgg tagcctctgc120
tgcaactgaa ctggcagctt ttgccgctgc ctttagctct gcattgtatgc gccctgaagg180
ttctgcctct ctgtttttgga atcgcccttc cctcctcatg tttggggacc tgcaagggtg240
tgaggcacgt gagggcatcg ccatgcgtat ttacaggcc tctttctctg gactgtcttc300
aaagggatga cttt                                     314

```

(2) INFORMATION ON SEQ ID NO. 37:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1839 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```

gcggggcagg gcggagcaac agagcggccg ggagtaaggc ggagtggag gaggagcttg 60
atggaaagcgt gcgagaagg gcgtaactga ttgggaaacc agaggaaagg cgctgttttc 120
accgaattag aatcgcgga aaatagagaa gagtttgttt gaagggtctc cgagatcgag 180
tgagtacggc tcgccaaagt ggagcgctct cgcgatagac acagcaacta ttcagctggc 240
agggggcggg agagggtgtg agcactctcg cgagatttga agggagcggc gagggcagag 300
ggaggagagg accggaagtc ctctatctca agcatccaat gctgaaacgg gcctgatttt 360
ctctaccgga agcccttttc cagagggtgg gaacacggcc cacctagcag gaagtccac 420
ctccttgagc tcgccacacc ttcccgaagt tttctgtca cctgtgttag gctcgtccc 480
ctttccgggt tttatcccg taccagaaaa ggatacatat agtgcctccc acccagctcc 540
actaaacggc ctcccgcctt cctgtgtgtg tggcgcgtgt gctgtgggga gggcccccga 600
cccgggggct cattcgagcg acccgggacc acaatgccag catggaattt gcagaccttc 660
cagctctgtt tggggctacc ttgagccagg agggcctcca ggggttccct gtggaggctc 720
accagacaaa tgcctgcagc ccatttgcgc caccaccccc agccccggtc aatgggtcag 780
tcctttattg cgtgcttcga agattcgact gcaactttga cctcaaggtc ctaaatgccc 840
agaaggctcg atatggtgcc gctgtagtac acaatgtgaa ttccaatgaa cttctgaaca 900
tggtgtggaa tagtgaggaa atccagcagc agatctggat ccgctctgta tttattgggg 960
agagaagctc cgagtacctg cgtgcctctt ttgtctacga gaaggggggt cgggtgtctc 1020
tggttcacga caataacctc ccttggggct attacctcat ccttttcaca gggattgtgg 1080
gactgctgtt tttggccatg ggagcagtaa tgatagctcg ttgtatccag caccggaaac 1140
ggctccagcg gaatcgactt accaaagagc aactgaaaca gattccctca catgactatc 1200
agaagggaga ccagtatgat gtcgtgtcca ttgcctgga tgaatatgag gatggggaca 1260
agctgcggtt actccctgt gtcctatgctt accacagcgg ctgcgtggac cctggtctca 1320
ctcagaccgg gaagacctgc ccattttgca agcagcctgt tcatcggggg cctggggagc 1380
aagaccaaga ggaagaaact caagggcaag aggaggggtg tgaaggggag ccaagggacc 1440

accctgcctc agaaaaggacc ccacttttgg gttctagccc cactcttccc accctctttg 1500
gttcccttag ccagctctcc cttgtttttc ctgggccttc aacagatccc ccactgtccc 1560
ctccctcttc cctgttatt ctggtctaat aacccccac acatacacct ctggtgacct 1620
atttgacagc accgtcgtct tcctccagtc cttctgaggg ataggggaca ttccatccca 1680
agcttctccc ttacccacac ctatcctttt gaggggcttt ggggtggggc tggggcaagc 1740
agagggactg ggtcttcact tcttgggcta ataaaaattg ttctttgttg actaaaaaaa 1800
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa

```

1839

(2) INFORMATION ON SEQ ID NO. 38:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1931 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

cagccgcgcgc ccatccctct ttgtgtgctt tggaaagccg cggagctggt ggtggctaca 60
gttgggtgttg ggggcttagg cgagggagct taccgggaag ttgcaggcgg gaggactctt 120
ccccatccag tcacctgaca ggtcacaaac atgtcagaca aaagtgaatt aaaggctgag 180
ttggaaacgta agaaagcagc actggcccaa atcagagagg aaaaagaagag aaaagaagaa 240
gaaaggaata aaaaagaaac agaccagaag aagggaagctg ttgctcctgt gcaagaagaa 300
tcagatcttg aaaaaaaaag gagagaagct gaagcattgc ttcaaacgat ggggctaact 360
ccagaatccc ccattgtccc tctcctctatg tctccatcct ccaaatctgt gaggactcca 420
agtgaagctg gaagccaaga ctctggagat ggcgcctgtg gatctagacg aggcactatt 480
aaacttggaa tggctaaaaa cagcgaagtc gactttccct ctcgagaaat tgtcacgtat 540
acaaagaaaa ctcagactcc agttatggct caacccaaag aagatgaaga ggaagatgat 600
gatgtagtgg ctcttaaac accctattgaa cctgaagaag agaaaaactt aaagaagaat 660
gaggaataatg atagtaaaac tcccctctat gagctgactg aagaagaaaa gcaacaaatc 720
ttgcactctg aggaattttt aagtttcttt gaccatttcta caagaattgt agaaagagct 780
ctttctgagc agatttaacat ctcttttgac tatagtggga gagatttga agacaagaa 840
ggagagattc aagcaggtgc taaactgtca ttaaatcgac aattttttga cgaacgttgg 900
tcaaagcatc ggtgtgttag ttgtttggat tggtoactct agtatccgga gttactcgtg 960
gcttctataa acacaatga agatgccctt catgagcctg atggtgtggc cctgtgatgg 1020
aatatgaaat acaaaaaaac taccocagag tatgtgtttc actgccagtc agctgtgatg 1080
totgccacat ttgcaaaat tcatccaaat cttgtgtgtg gtggatcata ttcaaggcca 1140
attgtgtctt gggatcaacc tagcaataaa agaactccag tgcaaaagac tccactgtca 1200
cgagctgcac acacacaccc tgtatatgtg gtaaatgttg ttggaacaca aaatgctcac 1260
aatctgataa gcatctctac tgatggaaaa atttgttcat ggagcttggg catgctttcc 1320
cacccacagg atagcatgca gttggttcat aaacagtcga agcagtagc ttgtgacatt 1380
atgtccttcc ctgtttgaga ttgcaacaac tttgtgtgtg ggagtgaaga aggtctgtgt 1440
taccagcatc gccgcctatg cagcaaaagc ggaatcagtg agatgtttga ggggcatcaa 1500

ggaccaatca ctggcatcca ttgtcatgca gctgttggag cagtagactt ctcacatctt 1560
tttgtcactt catcgtttga ctggcacagta aagctttgga caactaagaa taacaagcct 1620
ttgtatctat ttgaagataa tgcagactat gtttatgat ttatgtgttc acctaccoc 1680
ccagccctgt ttgctcttgt ggtatggcat gggagattgt atttgtgtaa tctcaataat 1740
gcacacagag taccaaactgc cagcatttct ttggagggtg atcctgcctc taactgtgtg 1800
agatggaccc ttctgggaag gggaggttgt tgtggcggga ttctgaagga caagttttgt 1860
tattttggga ttttggggag agcagtttgt tgggtccccc aatgatggat tggcgacggt 1920
tggcccgacc c
1931

```

(2) INFORMATION ON SEQ ID NO. 39:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```

agttaccatt gccttttctg tctcgtgccg gttttggttt gctgaaaacta gtccaaaaca 60
ggaaatttaa cagacagcca cagccaaaga gtgcatgtg aattacaaga aatagagccc120
atttagggaa agatagaact agaaggctt ttcattataa ttccatgttg aacaattgag180
tcatagcctc ttatcttggg ggaaggacac aattcaaag ggcaagtaag attttgtaaa240
acgtggcatc cataatttac tatggagcaa gtgccacat ctctaggaca ttaa      294

```

(2) INFORMATION ON SEQ ID NO. 40:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 882 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

tttttttttc tcattaacaa agcagtcgaat tccctttatt tttaaaattt tatgtacaca 60
tatgaatgat ctgtataatg tacattcaat atagaaagct ttatatattt gatagtgtat120
agaacatttc acaattacac tcattcttta cataacatct tgacatccat ttttaaattt180
ttttgcacaa gtcctctttc attcaatttg gtaaagccag ttatacatac taatgtgtac240
tgtgagcttt cagaagggtta atgattgagg atgccagtgga aggggtgcagg gacaaaacct300
aatagtcttg gatgggtggg ggaggatggc cagcgagact tgatgcagga gagggaaata360
ttctttctcg gggaaaaatg acttagccca atttttggtg actgtagctc aaccttacag420
tcacgctagt tcaaaaaaaaa aattacaaaa actaggaaga aagttttgtc tttttgattc480
acagttttgt aaacagatat aaaggaacaa atgtgcttac atacaccaag aaaaaaaaaa540
ttcttgtgta ccactttatg ttgatccaca gattgtcttc ttataatgtg atacaattag600
gatcaactgac tttttttcct aaaaatatat ttatagaaaa aggaataaca ctgtcatgaa660
accagagaaa aggcagtaag agtttgcttc aacgatcag ctggaggaat gtggactctg720
cactggcctt tcagcgctta ttgtctctcg tgaatatctc aagtctgata gccaaagtcg780
cctgcctcat ggtctacagg aggtggcagg ttagacatga ctgatgtaga tgtactcggg840
taaggtagcc agcaactcca ggtcctgctt cagagagctta ca 882

```

(2) INFORMATION ON SEQ ID NO. 43:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 934 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

ctcgccgccc acacagggag cagcgagcac gcgtttcccg caacccgata ccatcggaca 60
ggattttctcc gccccagccc aacggggagg gctagtgcga catagtgatt tagatgaaag120

agctattgaa gctttaaaag aattcaatga agacgggtgca ttggcagttc ttcaacagtt180
taaagacagt gatctctctc atgttcagaa caaaagtgc tttttatgtg gagtcatgaa240
gacttcagg cagagagaaa aacaagggag caaagttaga gattctagta aaggaccaga300
tgaggcaaaa attaaggcac tcttggaaaag aacaggctac acacttgatg tgaccactgg360
acagaggaag tatggaggac cactccacaga ttccgtttat tcaggtcagc agccttcgt420
tggcactgag atatttctgg gaaagatccc aagagatcta tttgaggatg aacttgttcc480
attatttgag aaagctggac ctacatggga tcttcgtcta atgatggatc cactcactgg540
tctcaataga ggttatgcgt ttgtcacctt ttgtacaaaa gaagcagctc aggaggctgt600
taaacctgat aataatcat aaattcgttc tggaaaaaat attggtgtct gcattctcag720
tgccacaat aggcctttttg tgggctctat tctaagagt aaaaccaagg aacagattct720
tgacaagaaa aaaaacagag gcttttgcct tcttgaatat gaagatcaca aacacgctgc840
ccaggcaagg cgtagggttaa ttgagtgga aagtcagggt ctggggggaa tgttggaact900
gtttgaattg ggggtgttcc gcttaggaag gtcc

```

934

(2) INFORMATION ON SEQ ID NO. 44:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 231 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

ctcgtgcggg tcaattatga gttcctttat ttattgggtga gaaagattag caagtatgac 60
gtatgcaagg aatagaagtt atgtaccgag tggttaaaagg ttgggggggat atggagatgg120
atgagaggga gctgtctggg aaggctttgc ttcaacttga tttagagtagg gttgcgtgaq180
gaaatagggtg tgtagaatga gaatgaggtt catgacagcc tctacaaaa c

```

231

(2) INFORMATION ON SEQ ID NO. 46:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

cgatcacgtt ttcacatgat gctcacgctc agggcgcttc aattatccct cccacaaaag 60
ataggtggcg cgtgtttcag ggtctctcgt ctctctccta cagaaaaaaa aaagaaaaaa120
atgtcattag aagaggcgta acacgtcagt cgtccccag gtttgtgttt cctggagtgg180
ccgaaagaga tcagttctaa cctgctctgc aggaataacg gtcctgcctc cagacactct240

```

(2) INFORMATION ON SEQ ID NO. 47:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

agagcagatc agaggcaggg gaaaaagcac gcagagggag gagctgaaga gctgagaccc 60
ggagccaggg acagcttaat gaagacaaac tgaaggggaa actgagatgc ttagaaagcc120
cagctataca actctaccga gaaatacttc ccttagggaa tgtaaaaagt actactggag180
atggaagagc agaaaaacag ctatgggcag aaggccaagg ggtgatatg      228

```

(2) INFORMATION ON SEQ ID NO. 48:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1229 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

aaaaaaaaa aaaaaagagt taatctagga gataatgaat ggcctagtag tagataatat 60
atggccccc aaagctcttga cttctgtcct tggggaaagc cattttgtta accacactag 120
tgagatttat atgatgtcta atggagaaca gagaagatct tgttgcaaaa ggtgtattaa 180
atatattgtgc tgtttctgta tgagattgag aagcttttcc cactctccac cctattttcc 240
tataaggata tccagagaag ccaaaactgtt ctgtgggttt gggaatggtc atttccggg 300
aaaatgcato tggatcgatg actaaacctg gcccttttct ctgggctgta gtgaagccgc 360
attttcacgc tggctggcag tgtgctgaga gccctgaatg ctctggcgcc tagtgcctt 420
ctgcccctgcc tgacgatgta tcgaaaagat gagagtgaag gagactttgt gcagcaggaa 480
acgggttagt gaggtgtgtg gcagttgttg gaactcttga gagtattaca gagtgttaga 540
atcggtaaga actctgattt ggaacttcgt ttggtggaac tgtgtgccta tacctgcctg 600
tgtgtgtgca agtgtgcagg ttccctttgta tgtatgtgta cgtgtgggaa cctgtgtttg 660
tcataattttt cttcatttca caaaggcctt ttttgaagca gtggcagtat gcccttggtt 720
caagaacaca tgaattcttt ttaacaccag attagtgtgt taccccaaat gaacggttct 780
agccctctat taagaataaa agggaccata agcatttttg ctgcttattg ctgtgtgtta 840
ctacttacaa gagtcttgaa aattatacag aactttgcct tcttttttta atgtcttcca 900
caatgttgtg actgattata accctgtttc cctccagaga agagctatgg ctcagggtatc 960
tgtgttgact ctggcattta gtggctttgt gaaggaaaga aaccattaaa tgacctgaca 1020
aaaactgact catgtcttta aagtgttgta agccactttt aggaatgtta cttctcggtg 1080
cttttgtcta attctaaatgg gcttaaaagcc aagaaaaacca tagtataaat ctttttgtgt 1140
taccctatgg ctagtgtttt aaatgggcag ttccgttgtg gataaagtat ccagtcactt 1200
caggtttccg tggaagggtt ttattgggg                                     1229

```

(2) INFORMATION ON SEQ ID NO. 50:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 231 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

gaggccggga gtggaacccc ctcttttgag aaggttgctt gactcagaga cacagaaacg 60
ggtccaggga tggggagaga tgtggagtga gggaagggtt gcatttgaga aaggaagtct 120
gagaacacac tgggacattg taacacattt gaaccattct ctgatatgaa ggtgttgcc 180
tcctaataat gggaggtcag gcccaggtcc tcgggcatag ggagagggtc c 231

```

(2) INFORMATION ON SEQ ID NO. 51:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

tttggcattca ttacaaattt catagaatta ctgtgaaggc ctttctagtt gagatgttgg 60
ggtattttggg attctaattg ttaaccccag aagaaggtaa tttagcttgt atttattttaa 120
aaccocattta gcttttttac tatatctggg agaattccag tgaatcatct aataaggrat 180
atttcagaaat aatttttttt tccttcagaa taacttagaa tcagatgcta taagggtctcc 240
tagggagcagt gtgaaatttc cgtaaagata aatttgaatg ttgtaaccaa gtttatatta 300
aaccagagg ccattttccaa tatgattttt tgtttctttt taacttgta agtccctaag 360
agattacatg ctagggtctg agtcatcttt attgtagata atgatggccc acacagtcac 420
cttcaactat ccacataagc taggcttttc gcttttgcca cggacagtg gaccaagata 480
tttccagagt aaataaccca ccacaacctt ggtaattcct cttttcttct taagctccag 540

gaagcgaaag cagaaggact cttttcagac tgcctctctg agcctacatt gcagctttcc 600
aaaacaggca gctagcactg gaaaagccca tgtgggtgac ccatattttt ctgaggttct 660
tcttttccat ggtgttactt tattatcaga aagtaaatcc agaaaacagg tcttgccctt 720
agcagacaag aaccacacca gtttcttgta aaggtaacgg atacattggg attcaggagt 780
gacacagagg tccagcccca gaacttghtaa ggattttgtt tgaacctga gcagatgcc 840
ctccctgcc acccatcaca ctagttaggg ctggccatga attctatgcc agagtcactc 900
ctgcagtcgt ctagggatgg gctttcttat cccactctcg cacacatccc agtctagtct 960
ttgccttcac agagtctctc ttgacacccc tgacttaatg atagtgtctg ttttgagatc 1020
gaattgatca ggtttaagtc atcctgctca ggttgggcac agtggctcat gccgtaatc 1080
tcagcacttt gggaaagcaa agtggggagg ttgcttgagc ccaggagttc caaacccatc 1140
tgggcacaag agggagaccc tgtctctacc aagaaaaaaa aaaaaaaa aagttaaaaa 1200
aaaacaattg ctggacctgg tgggtgcacac tcagtaggct gaggtgaaag gattcctttal 1260
acatggggga ctgaagatgc agtgagccat gaatcagcaa ctgcacacca gtatgagaga 1320
aaaagtggaa ccttatcaca

```

1340

(2) INFORMATION ON SEQ ID NO. 52:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 226 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

gccagatttc cggggttttg cgggcccgc gatgttttc agaggttttc aagtgggaag 60
aggagagcga caaggtgaaa atgccccgtg ccggggcgtc cagcggagtc ctgccagctgl20
tccggcggtg gggtggaagt ctgatttatg aaggtgccca tccacctatc tgaagtacctgl80
acttgtgagg actgacaact acagcatcag gtacaaagt gttctt      226

```

(2) INFORMATION ON SEQ ID NO. 53:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 611 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

gcagctgcag cggcagcagc ggcagcagag gcagcagcag tagccaccac tccgccgagg 60
cgcaaacccc ggctcgccct cccaggcccc cgccgctgcc gcagtcattg ctgctgatgg120
ggcggagcaa cgctcgccct tgcgtgcagc atcccactcc ggaaatgtca ctcccaccgcl80
cccaccgtac ttgcaagaaa gcagccccag agcggagtc caccctccata tacagccatt240
gccagtcag acgcccagtg tattccagta ataaactgcc gtgtgtgcc atcactaatc300
aatttgatg gcaagcttca ccagcatgtg gttaaagtca cagtttgcaa tgaagctacg360
ccaatcaaaa acccccacac aggcagaata tatgttagat gcccttgtaa ttgtcttctc420
atttgttaag acacatctcg gcgaatagga tgcacaagac ccaactgtag acggataatt480
aaccttggcc cagtaaatgt tatttctgaa ggaacaacca gctcagccgt cattgcccac540
tcccaccag aagggtacaa gggctgtgtg ttggggcacg gttggggaac acattccctt600
tgggatggga c

```

611

(2) INFORMATION ON SEQ ID NO. 54:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 689 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

gcgcagccgga cgcagggggc tggcgggaac gtgaagctcc gcgggtccgt atggggccgt 60
tggggcgccg gtacgtgttg ctgttggggg accccctcat tccctgccgt gccgtccctg120
ctgcctcatg gcggccatcg gaggctcacc gggtgcacc tcagcctgtg tggccgtcta180
taaggatggc cgggctgttg ttgttgcaaa tgatgccggt gaccagatta ctccagctgt240
tggtgcttac tcagaaaaatg aagagattgt tggattggca gcaaaaacaaa gtagaataag300
aaatatctca aatacagtaa tgaaagtata gcagatccgt ggcagaagct ccagtgtacc360
acaagctcag aaatacatcg cggaaagtta atgtttagtc attgaaaaaa atgggaaatt420
acgatatgaa atagatactg gagaagaaac aaaaattgtt aaccagaag atgttgccag480
actgatattt agtaaaatga aagaaacggc acattctgta ttgggctcag atgcaaatga540
tgtagtattt actgtcccggt ttgatttttg agaaaagcaa aaaaatgctc ttggagaagc600
agctagagct gctggattta atgttttgcg attaatccac gaacgctctg cagctctctt660
tgcttatgga gttggacaag actccctta

```

689

(2) INFORMATION ON SEQ ID NO. 55:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 560 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

agaaaatgga cgctgacatc aatgtcacaa aagcggatgt tgaaaaggcc cgacaacaag 60
ctcaaatacg tcaccaaatg gcagaggaca gcaaaqcaga ttactcatcc attctccagal20
aattcaacca tgagcagcat gaattattacc atactcacat ccccaacatc ttccagaaaa180
tacaagagag cggaggaaaag gaggatttgt agaattggag agtccatgaa gacatatgca240
gaggttgatc ggcagggtgat cccaatcatc gggaaagtgc tggatggaat agtaaaagca300
gccgaatcaa ttgatcagaa aaatgattca cagctggtaa tagaagctta taaatcaggg360
tttgagcctc ctggagacat tgaatttgag gattacactc agccaatgaa gcgcactgtg420
tcagataaca gcccttcaaa ttccagagga gaaggcaaac cagacctcaa atttggtggc480
aaatccaaag gaaagttatg gccgttcac ccccaaaaata agcttatgtc ccttttaacg540
ggggggcccat tcagcttcag                                     560

```

(2) INFORMATION ON SEQ ID NO. 56:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 851 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

gaagaagagt aagaaggaca agaaggccaa agctgggtctg gagagcgggg ccgagcctgg 60
agatggggac agtgatacca ccagcaaaaag aggtagaatt ggtttctgag tagtgaaggc120
cacttgaagc tggaggagaa actaaagcct tattgagaaa acatgttata gatccttttg180
ttgctgagag agtggaaacat aggtcctaga cagggtgaa agttctggca catttttagct240
gctactttga gacctcggtg atgttacctg gtgtgggtcat cccatcttgt cctgttttaa300
ggatatgggt ggtgaaagat gaaagaggca gagtttatcc caatgaactc tctgtttgag360
ttggggaagc tcaccttcag acccagtaac tgtccgcagc tgtctgctag tggttgtctt420
aacatcgtag tctctagttg cattttttaa atccctctg tttaaaagg tgtgaaaaca480
aaaaacaaaa actaagtctg ctcaagtcaa tgctgtagaa ccctaaaataa gtggtagaag540
agtgtcactg aattttgtct ctgaattcag tataactgag ttttgtccat gctgggtgtc600
gggttatagg cctgatgggc ctggtagttt tccatcttgt tctggcctag aggtcagtc660
tttgcacttc ctcaaaagctt gtgtacagtg ctcaactaaa tccatctgac tacttgttcc720
tgtgccctct tgttttaggc ctgcgtttact tttaaaaaat gaaattgttc attgtcggga780
gaagaatggt gtaattttta ctctattaaag tcaacttggt aagtttttaa aaaaaaaaaa840
aaaaaaaaaa a                                     851

```

- (2) INFORMATION ON SEQ ID NO. 57:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1354 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

cttaccaca gctttctgc taagtctgt ttttggata tttatgactt ggttcattctt 60
attttttcct gatttagcag gagccccctt ctatttccagt ttcattttca gcatagtagc 120
ctttctatac tttttctata agacttgggc aactgatcca ggcttccacta aggcctctga 180
agaagaaaaa aaagtgaata tcataccctc tgcagaaact ggctctctgg acttcagaa 240
attttgtaca tcagtgttta taaggaaaggc attaaggcca ctccactgcc atgtatgcaa 300
ctgctgtgtg gctcgatatg atcaaacctg cctgtggact ggacgggtgca taggttttgg 360
caaccatcac tattacatat tcttcttgtt tttcctttcc atggtatgtg gctggattat 420
atatggatct ttcattctatt tgtccagcca ttgtgccaca acattcaaag aagatggatt 480
atggacttac ctcaatcaga ttgtggcctg ttccctctgg gttttatata tcttgatgct 540
agcaactttc cattttctcat ggtcaacatt tttattatta aatcaactct ttcagattgc 600
ctttctgggc ctgacctccc atgagagaaat cagcctgcag aagcagagca agcatatgaa 660
acagacgttg tccctcagga agacaccata caatcttggg ttcatgcaga acctggcaga 720
tttctttcag tgtggctgct ttggccttggg gaagccctgt tgggtagatt ggacatcaca 780
gtacaccatg gtcctttcac cagccaggga gaaggttctt cgctcagtat gaagaaaaagc 840
aaccacaaac tctcaatctg atttgttttt gtttatgtcg atgccctgta gtttgaagat 900
gaagtaaaag tttagaattc acctaaagtc aaaggaaaaa acgtgggtttt taaagccatt 960
aggtaaaaaa agttctcaat aaaggcatta caatttttta ggtttagaaa gatggacttt 1020
tttgataaat cttggcgacac atctaaaaaa aaaaccatat ttttcacaag aaaatgcaag 1080
ttactttttt tggaaataat actcactgat tatggataaa atggaatatt ttcagatact 1140
atatggctg tttcaaaaaa gtactattct ttaaacctgt aatttttctg aagttatttg 1200
tctttgttgt atctataaat atgtaaaaaa tatttaaaata gatgtacctg ttttgcctttc 1260
acacttaata aaaaaatttt ttttgtaaaa ggaaaaaaa aagaagagga aaaagaagag 1320
aaaggagagg ggaagaaaga ggagaaggca agga 1354

```

(2) INFORMATION ON SEQ ID NO. 58:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 268 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

cgtgatctct cctcagtaaa accaaggtgc atttttctgg acccacctat cttgggggtg 60
attaggagta gagggttgta aatacttaaa atttttttcc ttctgatat aattattgat120
ctccttctag aagtctctgtc gtccttgctg gagaattttt attttaagcat cctttttagt180
aagaatctct aatgtccctt tttcatccag atctacactt gatgaatcct aaagctattt240
ctacacagtt cctttattca gttttccc

```

268

(2) INFORMATION ON SEQ ID NO. 59:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 752 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

tgacaaaaga aatggaataa ttccaaaaaa gttaagtcct gagaagacaa ccctgaaatc 60
tattttgaaa agaaaaggca ccagtgatat cagtgatgaa tctgatgaca ttgaaatttc120
ttccaaagtca agagtaagaa agagagctag ttcatgtagg tttaagagaa taaaagaaac180
caaaaaagaa cttcacaatt ctcccaaaac aatgaacaaa acaaaccaaq tgtatgcagc240
aaatgaggat cataactctc agtttatgta tgattatcca tcttcagatg agagtttatc300
cgtcagccac ttcagtttct ctaaacagag ccacagacca agaactataa gagacagaaac360
tagtttttct tcaaaattgc ctagccataa taagaaaaat agcactttta ttccaagaaa420
accaatgaaa tgttcaaatg aggaaagtgt ttaatcaaga gcagtcgtat gaatcaattg480
ataaaatttt agatggcgtt caggaaagtgg cttatatcca ctcaaacag aatgtaattg540
gatcgacgaa agctgaaaat cacatgagcc gatgggcagc acatgacgta tttgagttga600
agcagttttc acagctgaca gctaacatag ctgttttcag ttctaagaca tataaagaaa660
aagtggatgc agatacattg ccacacacaa agaaaggcca gcaaccgagt gaaggcagca720
tttccattcc tctttacatt tcaaatcctg ta 752

```

(2) INFORMATION ON SEQ ID NO. 60:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 1389 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

gaactccaag ttagtggatt gcagaatgga aacttggctt ttggggcact gggtagattt 60
tagttttgtg gtgtcttgct ggggggtggt gatgattgtc tcagcactca cgcactgcac 120
aagatggcag caggatcacg cactgcacaa gatggcagct cctctgcagc ttccctcctc 180
gcctccctcc ttgcaccccc acaggttttg cttgggtttt ttgtcatcag taacctactg 240
cctgagatca tgacctctta aaagatgaga ccttcggaag ggttgattgt atgcgtcagt 300
gagcctctta tcaccttctg gaacaaagtc acttgaaatc tcttgatgag attaaaggat 360
ttagtgttac taagaaaaatc tgctttgggc cgcagcagtg ctgggtgttc tcagacctga 420
ctgaggaagt tagctgcggg ctgcccctgt ggtggtgct tcagagagaa tccagagaa 480
tggtcagatg ccccccttgg gctccttctt aatcttaac agctctttaa atagctgcc 540
atctcctgtg attgcacaac caagcacttt gacatttgca ccttaggaga ggcagatgtt 600
aaaaatggaat ccaaaagacca cctaggggcg ggttgggtgg gagatgggag ggccaactgc 660
gagctgtctc acttctcagc tctccccctg cctgcagccc tgggcccagc aaggccagaa 720
ggtttcaggg gcatttgaca tccccctctg gttctcacca ggaaaaacac caaagctttg 780
gaggaaaacag gccctgcccc tggctcctta aatgcccgtt ctcttcttaa actgatattc 840
agccagcaat gccataagact ttgttaagat catttctact gctttctttt ctgcttcaaa 900
cacacagttc gtctctgagc aaagtaaaat aatggaata agagttaaatt gggtaaggag 960
atatccaaag ctaccagtc ccttgaccca gcacagttgg ccgacccgtg tcaactccctg 1020
gctgtcgtgt cttctctgtg ctcactgaag ggtgagccag gccagtgtct cccacgcccc 1080
tgggcctggt cactacacag tggaaaaacag acaagcggcc ctttcccaaa atcccaagag 1140
tgtcttctgt cttgggtggg gctcatcgca atgttctgaa ggctccaggg ccactttgtt 1200
tgtaaagtat attcgggccc caaaatacca tagtagctgc ttgataaaat tctaaaaaat 1260
tctggttctc tattatgtaa acactattac agtcaccagt ggtgtaagac ttttgagtct 1320
ggttctcata tcagagtcat catttttctt cctgtggaat aaaatgcctt gggactcccc 1380
caaaaaaaaa

```

(2) INFORMATION ON SEQ ID NO. 61:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 726 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

```

cgtatctgtc cggacggaag caggaagcgg gagcggttag gccacgcctg cggcgctgct 60
ggttgaggct gtgtgggtgg gggacgggccc gaggcgatgg cggagaagtt tgaccacctal20
gaggagcacc tggagaagtt cgtggagaaac attcggcagc tcggcatcat cgtcagtgac180
ttccagccca gcacccaggc cgggctcaac caaaagctga attttattgt tactggtctta240
caggaatttg acaagtgcag acagcagctt catgatatta ctgtaccgtt agaagttttt300
gaatatatag atcaaggtgc aaatccccag ctctacacca aagagtgccct ggagagggct360
ctagctaaaa atgagcaagt taaaggcaag atcgacacca tgaagaaatt taaaagcctg420
ttgattcaag aactttctaa agtattttcc gaagacatgg ctaagtatcg aagcatccgg480
ggggaggatc accgcctctc ttaaacagct caccctccct gtgtgaagat cccctgggac540
tgcgatgcgg cgtgaggctg ggactgcgag tgctgacgcc acctcctctc tgagggtggga600
ctgggcccctg gacacacccc tcagccccctc tgcctcatt gtttgccctc atgggaccga660
ggggctggag gagagggcga gtgtgcccac gggttcaaga ggttggtttg ggtgaaatgg720
gtttgt
726

```

(2) INFORMATION ON SEQ ID NO. 62:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 681 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

ggctgagaaa aatggggggga gacataaacac ccacgaatga aaatacagat ttaagagaag 60
gaaccagttaa agtaggagac agatgtgaag gaaatggaaa tgaggcgaaga ggacattgga120
agaagaaggt ttgtgtttaa ggaagcaggt ctggagcatt agtvtgaggg agttcaggta180
ggctggggctt gtgcctcttag gtaggggacaa gggaggcttg gttagccaggg ctgggtgctta240
aaaccccttga ggcctatgagc tcattggctg cctttgtatg atcctgtctt cttctgtgt300
gctgtgtgtt atctcatctc acctggatbc aaagggttaa gtgggcatgg gtcttggggc360
tgacacccca caaggatgac ctgtggactg ccactcggatg ctgaacaggg agatgaaagg420
aggttcctctt acctatcccc tctgccaaac cccagtagtg ccactgttct gactttgttt480
ccagaatata cagaaatcca aaggggctgt tgcgtgaacag tctgcaggac cagtgcagcg540
acctacctgt tgtcccaagg catcaaaagg aggcctcaac gctcatgctt ctctaataca600
gccctaccac gacagacaga aaaggaaagg gttagaggaga aggttgaaac tgtggaggtta660
gacctctgctt cattcctgaa g
681

```

(2) INFORMATION ON SEQ ID NO. 63:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1116 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

ggggccacact gaggcagattc ttgtgtagaa ttttcaactt gagactaaca caagtatattc 60
cttttctgtt cagttctcca aatgacaaga agtctttttg ctcaattgaa ggggaatgga 120
atgggtgtgat gtatgcaaaa tatgcaacag gggaaaatac agtcttttga gataccaaga 180
agttgcttat aatcaagaag aaagtgaaga agttggaaga tcagaaacag tatgaatccc 240
gcagcctttg gaaggatgtc actttcaact taaaaatcag agacattgat gcagcaactg 300
aagcaaaagca caggcttgaa gaaagacaaa gagcagaagc ccgagaaaag aaggagaagg 360
aaattcagtg ggagacaagg ttatttcatg aagatggaga atgctgggtt tatgatgaac 420
cattactgaa acgtctttgg gctgccaagc attaggttgg aagatgcaaa gttttacct 480
gatgatcagg gcagtaggca taattcagca acaaaacaatc ttcttttggg agaaacctgt 540
tcattccaat cttctaatta cagtgggttc tatctcagg atactggact ttctgacgca 600
gatgaacaat taaggggaaa agcttccctt ttccctctgt ggcagttaac attttgactt 660
cagtcctgag aaaaacttca ggttttgaaa atcagatgat gtcttctctc ttcccaaa 720
ccacacgttg aaagcattta taaatccaag tctgaaactc tgcgctctag tactgtgtgt 780
aagatacacac actgttttct tagttcatat aatctcgagg acacacatac gtatacacac 840
acatacatat atataaatat acctgatgcc agattttttt cataaatatt ctgcctactg 900
taaatatggg ttctctcag trgttttaga aaattagcgc aatgtattaa aatcaagtgt 960
taggaaaattt ctatggctta ctacaataa cttttatttt ggaattgaac tattattaaa 1020
ttgtatctaa tcttggaata cagtttaatt aattattctt agtgcttaag gcttcataaa 1080
gtaatttttc caaccttttt tttaaaaaaa aaaaaa

```

(2) INFORMATION ON SEQ ID NO. 65:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 806 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```

tccaagggct ctttagtcoct tcttaagccc cacagtaact tcccgtagtc ctgagggttg 60
ggacctctcg gggttcttac ctccctccc cattgctgag acagtctgag aagaggcttal20
ggaatttgct tgtgggagtt tattcatctg tctctctat ttacctctcc caaaccaggal80
tttccacttc tcaaacctgc tgtgatctca caactggagg gagggaagtga gctggggggc240
tcattctccac tggctgcagg aacaggcctc cagggtctcc agactgatat tcagactgac300
aatgatttga caaaggaaat gtatgaagga aaagagaatg tatcatttga acttcaaaga360
gacttttccc aggaaacaga cttttcagaa gcctctcttc tagagaaaca acagggaagtc420
cactcagcag gaaatatataa gaaggagaag agcaacacca ttgatggaac agtgaagat480
gagacaaagc ccgtggagga gtgtttttt agtcaaaagt caaactcata tcagtgtcat540
accatcaact gagagcagcc ctctgggtgt acaggattgg ggaatccat cagctttgat600
acaaaactcg tgaagcatga aataattaat tctgaggaaa gacctttcaa atgtgaagaa660
ttagttagagc cctttagggtg tgactctcaa ctattcaac catcaagaga acaacactga720
ggaaaagcct tatcagtggt cggagtgtgg caaagcttcc agcattaatg agaaattaat806
ttggcatcag agacttcaca gtgggg

```

(2) INFORMATION ON SEQ ID NO. 67:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 226 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

gcgggataccgg cgttctctcac tgatcttttc caagggtgta cagagatggc gccgggtttt 60
cggaagcgcg gtaagtcctcg gacgcgggaa cacagagagc gaagcgaagt actaccgtaal20
aatacaaaagt acctcaaaag ttgttcggaag caagggtgtg aaaaaatac agtgagttct180
aaaacaaaat gactcggqtt aaactcgaag tqgggtatca aaaaaat 226

(2) INFORMATION ON SEQ ID NO. 69:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 2042 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(B) TYPE: Nucleic acid

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

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gcagccgtcg ccttcggagc gaaggggtacc agcccggcag aagctcggag ctctcggggg 60
atcgaggagg caggcccgcg ggcgcacggg cgagcgggcc gggagcggga cgcgaggagg 120
agccggcagc agcggcgcgcg cgggctccag gcgagggcgt cgacgcctct gaaaactctg 180
gcgcgcgctc gcgccactgc gcccgagcgc atgaagatgg tcgcgcctgt gacgcggctc 240
tactccaaca gctgctgctt gtgctgccat gtccgcaccg gccacctcct gctcggcgct 300
tggtatctga tcatcaatgc tgtggtactg ttgattttat tgagtgccct ggctgatccg 360
gatcagtgata acctttcaag ttctgaactg ggaggtgact ttgagttcat ggatgatgcc 420
aacatgtgca ttgccattgc gattttctct ctcatgatcc tgatatgtgc tatggctact 480
tacggagcgt acaagcaacg cgcagctgga tcatccatt ctctgtttac cagatctttg 540
accttgccct gaacatgttg gttgcaatca ctgtgcttat ttatccaaac tccattcagg 600
aatacatacg gcaactgcct cctaattttc cctacagaga tgatgtcatg tcaagtgaac 660
ctacctgttt ggtccttatt attctctctg ttattagcat tatcttgact ttaaggggtt 720
acctgtattg ctgtgttttg aactgctacc gatcacataa tggtaggaac tctctgtatg 780
tctctggtta tgttaccagc aatgacacta cgggtgctgct acccccggtat gatgatgcca 840
ctgtgaatgg tgctgccaaq gagccaccgc cacttaactg gtctgcttaa gccttcaagt 900
gggcggagtg agggcagcag cttgactttg cagacatctg agcaatagtt ctgttatctt 960
accttttgcca tgagcctctc tgagctttgt ttgttgcgtgaa atgctacttt ttaaaatttat 1020
gatgttatt tgaactctgt agttttccac atatgtcttg ctagaacact gtgatagatt 1080
aactgtagaa ttcttctctg acgattgggg atataacggg ctccactaac ctccctagg 1140
cattgaaact tccccaaaat ctgattggac tagaagtctg cttttgtacc tgcggggccc 1200
caaatgtggc cacttttctc tctgttccct ctcttttgaa aatgtaaaat aaaacaaaa 1260
atagacaaat ttcttctcag ccatccagc atagagaaca aaacctatg gaaacaggaal 1320
tgtcaattgt gtaattcatg ttctaattag gtaaatagaa gtcccttatgt atgtgtttacal 1380
agaatttccc ccacaacatc ctttatgact gaagttcaat gacagttttg gtctgtgtgt 1440
aaaggatttt ctccatggcc tgaattaaga ccattagaaa gcaccaggcc gtgggagcag 1500
tgaccatctg ctgactgttc ttgtggatct tgtgtccagg gacatggggg gacatgcctc 1560

gtatgtgtta gagggtggaa tggatgtgtt tggcgctgca tgggatctgg tgccctctt 1620
ctctcggatt cacatcccca cccaggggcc gcttttacta agtgttctgc cctagattgg 1680
ttcaaggagg tcatccaact gactttatca agtggaaatt ggatataatt gatatacttc 1740
tgcttaacaa catggaaaag ggttttcttt tccctgcagg ctacatctca ctgcttttga 1800
cttccaagta tgtctagtca ctttttaaaa ttgtaaacatt ttcagaaaaa tgaggattgc 1860
cttcttgtta tgcgcttttt accttgacta cctgaattgc aagggatttt tatatttca 1920
ctgtttcaaa agtcagcaac tctcctgttg gttcattatt gaattgtctg taaatttaag 1980
tagttgcaat taaaacaagg tttgccacca tccaaaaaaa aaaaaaaaaa aaatgggtgg 2040
cg
2042

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(2) INFORMATION ON SEQ ID NO. 72:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2980 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

| | | | | | | |
|--------------|------------|-------------|-------------|-------------|-------------|------|
| cagagtgta | gcgcagaa | cctcctgtgt | ccccagcctt | agagagctcc | cattctcaac | 620 |
| attgagctga | aaggctctaa | gcccaaaagt | gcacaacgac | ccccagctcc | cattcttcag | 120 |
| ctccctcgtg | gcgcagtgat | cctgttaaog | ctgtggaggt | cagctctgagc | taccaagact | 180 |
| ctccctagac | aaagctggag | ctccccacac | tgccccaacg | caaatccact | actcaacctc | 240 |
| ctgaggtgtg | gatggggcaa | cagagccaaa | actgagcagc | ctgatgcatt | cagcctgctg | 300 |
| tgccagagctg | ccatttgaet | ccctgatgtt | cagagagaaa | cgcacaaaac | gattgtcccat | 360 |
| gacatttggg | gcagcagatg | ccaagcagtg | ctgttatgtc | gttttctctg | gtgtatgaat | 420 |
| caggaaagctg | tgtgtgtotg | gaggcocaett | ctgtgttaatt | cttttccocat | ctgttcgaat | 480 |
| ttttagaaatg | cttacctctt | ggacagtgca | ctgtcattta | tcagagcact | attgtctagt | 540 |
| ttctctctct | ggcttctgtt | ttctctggag | agttttagat | tggggagcct | attctccatg | 600 |
| gcgcacaaaa | atgatgttca | gtgattcaat | taactaacac | caatgatctc | tggtgtctgg | 660 |
| ggggacagcc | ataagcaaga | catgcccagg | gtttgcogtg | gctccagatc | tactccctgt | 720 |
| aggagtctcc | ggatcacaga | caacgttagta | accaggggtg | tgaaatctag | tacacccttg | 780 |
| caaggctgtc | cttcagactg | aagcagcaat | cttgccacta | cagcagcaac | ccaggagctc | 840 |
| tggtttttgt | ggggggcaga | tcagaagaga | gaggcccgcc | tgatcccgcg | gctgcttggt | 900 |
| ccacaactct | tcocattcaa | ggatgtttat | ggcgcctctc | tgatcctctc | gtgagacaaa | 960 |
| tacagaaatg | accocattcc | tgccaccagc | aaactcagag | gtgatgtggg | agactgacac | 1020 |
| aggaaaaatg | actctaatac | gcagacatgt | gatatgtgtg | aagaagaatg | tgaggggagtg | 1080 |
| agagatgaat | tttccctgga | gggatcctag | aaagcatttg | ctgatgtcca | ttcccatatg | 1140 |
| ctccactttta | aaacaatagt | gtgtgtgaag | aacctttgtc | tcagggtagt | tcacagctgt | 1200 |
| aaataacttg | aaattttcc | agagttctca | aactctctac | ttccccaca | gatcacacat | 1260 |
| caagctcaca | aataggagta | gcaattctag | gtgttagggg | tgtgtacgga | accctctggt | 1320 |
| | | | | | | |
| gtctgcata | actccagaat | taccccagga | ccattgtccc | aaagtctaga | gtcttttcag | 1380 |
| gtaggcacaat | tttgttttca | atcgttgttg | ctcagctgtg | gtcacaaata | cccatcttag | 1440 |
| gatcccatcaca | gcttcccatc | ccccacagca | cagccacagt | accctccatt | ttctcccttt | 1500 |
| gttctttctca | atctcgttct | gcagaaagaa | actgccacta | attcatccac | actcaagttg | 1560 |
| aaatgatgtga | taataggaa | gagttacctc | ttccacacga | catttgtttg | taagtatgac | 1620 |
| agacagagctg | cttaatccca | agggaaaagc | ttatggacat | ggaggggggg | agctttctg | 1680 |
| gtagaagagct | acttccctga | tttccctaaa | accocagtaag | agtaagaact | tggttttggt | 1740 |
| aaggtctcgtc | ccacactcca | agagcagctc | tttttttttt | gtgtgtgtgt | gtgttaacgg | 1800 |
| ctctgaggga | atatagtaaa | aatgcataat | cagctgcaat | ttgcacggga | gcaatttccac | 1860 |
| catgtgtgac | tgatatggta | aatgtgtttc | ctgtgttttc | gatccaaaac | ataataacal | 1920 |
| ctatccttca | tcatagtttt | ttcaggggtg | ctgttgtatt | agtagggaat | ttgaaacac | 1980 |
| tttttaaaat | cagctcagaa | ataaaaacaa | ttgtttaaag | cacatttgca | tcagtagcca | 2040 |
| gctcacgcga | tttgtatata | tcocaaaagt | cattgtatgc | tcocaaactt | gctgcctttt | 2100 |
| aataaaatct | ttgtgtaaaa | tttgtcatca | gtgcctcttc | tatgtatgat | gaaacaaaga | 2160 |
| acagagattct | ccaattgtct | tttgtctctc | agacatttag | taatataaag | tacctatttt | 2220 |
| tatgcctgaaa | ttgtttatca | ttgtttatgt | tcagcaagtgc | actcaactgt | cgcgatgctt | 2280 |
| tgcaacacat | tttgtatata | tagccatgct | tcgggtgtaa | ggcagccccc | aaactccctca | 2340 |
| totttttgtat | ctctctcggg | atcagttaaa | gaaacaaata | ataatgtgct | taagaagtg | 2400 |
| gactgtgaat | ttgtataatt | aatcttgtat | agccccatga | cctcactata | atagaaaaat | 2460 |
| tttttttaaaa | atttgaatgt | aaaggggtta | aggaggttat | gaagtttttt | tgacttttaz | 2520 |
| taaaatgata | ggaattccaa | atgcactcac | tacagattct | tagcacaata | atgacattct | 2580 |
| taaaagtgtta | aaatttcaga | taagtattct | attggggagg | aaaggttaact | ctgatctcag | 2640 |
| tttactgttt | ttctttccct | tttaattttt | tttttgggtt | ttcttggttt | tgcagtccca | 2700 |
| ttctctgcga | ctgtgattaa | ctctcatatg | tagaataggt | tactacaata | agggttatct | 2760 |
| cttgaaagaa | aaataacatg | catatataat | aacccaattaa | tttaagatag | tgccatttaa | 2820 |
| attcacacat | gagagcaatg | cctatgcaga | catagatttt | ttctgtctat | ttttttctct | 2880 |
| cattgcagtg | gactgatttg | ataaataagt | grgttgtaat | actacatttg | ctgtacatat | 2940 |
| tttttaataa | actttattca | gaattcggct | gcgaataaaa | | | 2980 |

(2) INFORMATION ON SEQ ID NO. 73:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 227 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

cagcattgct ccacggcaca gcataaggat agatcccaag tccacagggt ccattttgca 60
gggtcatattc tgatcctagg aaatgtcctt ttcccatagt tgtcctatgc ctttggggtt120
tagtctatcc caggggtaac tgtggagaaa tcattgggtt gagagtcaag agagcattgg180
ttttggagct ttaatccctt tctggttgaa ataagggtgt caacttg                227

```

(2) INFORMATION ON SEQ ID NO. 75:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 773 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```

cggaagtgtta aaggtttctcg cctctctctcg gccaggcgga acctctctgc tgggcccgggt 60
ggcgcaaaaa gaacttttctt ttctccgccc gaacgggtgc cgcgcccaac tgcctcgcccl294
gcctggcagc ctaacctctc ttctcttctt ctctctctcg gcttcgcgcg gccctgcctc180
cctctcgccc ggcggcatcc gcttgctgct gccaccgctt cctcatcttc tgcccggcca240
accggcctgc cccgctgcag tgatgtgcga caaggagttc atgtggggccc tgaaaaacgg300
agacttgatg gaggtgaaag actatgtggc caaggagaa gatgtcaacc ggacactaga360
aggtgggaag aaacctcttc attatgcagc agattgtggg cagcttgaaa tccttggaatt420
tctgctgctg aaaggagcag atattaatgc tcagataaaa catcatatta ctctcttct480
gtctgctgct tatgagggtc atgtttctcg tgtgaaattg ctctctgcaa aggtgtctga540
taagactgtg aaaggcccag atggactgac cgcttttgaa gccactgaca accaggcaat600
caaaagctct ctccagtgat ggatggatgg actgataact ccggaagaat gactctctg660
tggcctcaca ctgctgcctg tctgtctgtc actctctatc tgcacagctc ttcagctaaa720
tacttttaaga ggggtgaggg gagagagaaa ttcataacaa atccgactac cag 773

```

(2) INFORMATION ON SEQ ID NO. 77:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 870 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

```

gacccggcgt ggctactagg agaaggacgt acggctctgc tagtagagga atatgtcag 60
ttttctctagg gcgccccagc aatggggccac ttttgctaga atatggtatc tcttagatgg120
gaaaactgcag ccacctggca aactgtctgc tatggcatct ataagacttc agggattaca180
taaacctgtg taccatgcac tgagtgaact tggggatcat gttgttataa tgaacacaag240
acacattgca ttttctggaa acaaatggga acaaaaagta tactctctgc atactggcta300
cccagggtgga tttagacaaq taacagctgc tcagcttcac ctgagggatc cagtggcaat360
tgtaaaaacta gctatttatg gcatgctgcc aaaaaacctt cacagaagaa caatgatgga420
aagggttgcat ctttttccag atgagtatat tccagaagat attcttaaga atttagtaga480
ggagctttctt caaccacgaa aaataactaa acgtctagat gagtacacac aagaagaaa540
agacgccttc ccaagattgt ggaactccacc tgaagattat cggtctataa agaataagaa600
ttgcagaaaa taacagtgaa gtgattgaaa ctctctctctg atgagtttct ctaacctaca660
ggatggagta aaacaactgc tacagttcag cactgttttt atgtgccgaa tcactgtgg720
gaaaagctga gaaggtgtag tccctcaata gaaaattgta attaaaaat aattttatag780
aacatttttt atgtaactct atttgaatgt tatagttgat aataataaaa tcacttact840
ggttgactaa aaaaaaaaaa aaagtgcagc 870

```

(2) INFORMATION ON SEQ ID NO. 78:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

ttgtgatcgg ctatccttcc cggatcaaca gcgagcccag cccggtcatt tacaaccggc 60
 ccgggaacaa cgtgaaactg aactgcattg ctatggggat ttccaaagct gacatcacgt120
 gggagttaac ggataagtcg catctgaagg caggggttca ggctcgtctg tatggaaacal80
 gatttcttca accccaggga tcaatgacco attcagcatg ccacaaagag gggtggc 237

(2) INFORMATION ON SEQ ID NO. 79:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 439 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

```

gtttgggaag ttgagatttg gagcgaataa gtagggatct ggcaagagga tcctctacct 60
cagtcattag gatttcttaa taaaaaagag attgtatttt tgagtgggtt attaaagattal20
ttaaaattag cccttccttt gaaatatgac atcagctttg ctgttctaaa tttaaaattal80
gttgcttcat cagtagcaca cttccagttt ctataccaag ccagtcttct cagttttccc240
cttaggatgg gacaagtctg ttcagggggt cattctgtaa gggtcagcag ggggtttggg300
agaggattta aggggaaata cagtgggggc agaatgggtt cgggggtaaa ggtaggggac360
aagggaggga ggccgaaagg aggggtggaa ggatgggggc cttacctaga tcgggggatg420
ccgggggggc aaggcaagg                                     439

```

(2) INFORMATION ON SEQ ID NO. 80:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2483 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

```

gcaaaagtct tcaaaactatt gagaagaagc catagactga gtgcaggcac cagtgcgctc 60
ttattactgt gtcaattataa tgaatgtatt tgaatgtttg gatacttacc tctgaatgta 120
tttttagtaa taacttcaag tgcaaatatg gccatgcata atttctttgg tctcatgttt 180
ttcccccttc ttcttttagg ctttgtcttc tgagtctata gaaaaacttc cagtttttaa 240
caagtcagcc ttcaaacatt atcagatgag ctctgaggct gatgactggg gtatcccaa 300
cagggaaoca aagaacctgg caaaagaagt ggccatgtga agagggacac tcaggacact 360
ttacgggatac aaagtgggtc tacaccaagt ctgcttctcg aatgtttgtg tgtgaacct 420
tgtttctccc aaaaacaaag acagcaacga aaactcotta atcagaacac tgatccaatg 480
aggaatggag cttgtttctg tgacccagga gaacttagtg caagactaca ggagttaaca 540
gatggccagc tcttattttt ttaattgtaga ataactcctg agtttatatc aaatcctgaa 600
gaaataagcc tcagttttcc atctgttttt gataagaata agaaagggag tgagtgtgaa 660
gatggtgtgt agcagtttca ctaagactga tatttttagc ctctttgtca catcaaaaga 720
tattgtgtgc agaataccag cattttctcg ccactgcaag gattaaact tagtttacac 780
tatgtgggtc caaatatatg tcaatgtaca ttttgaacat atttatgtgc tatggaaaga 840
aatgtcgttg actaaaataa ggtttactct gaaagaggag gaattttatt caaagcattc 900
aaacattttt ttcaagtgtt tcaaaatcca aagcatttga ttcaaaagtg cagtgaaggc 960
atcaactttt gtaaaaactc agaaaggaag ctctctctgat aaaaaacacg ctcttttatt 1020
atgctgcttt tcttgttcac tttaacacac aagtaaacac ttattgtcag gtgcctagtc 1080
ttgagtgaat tgttagatgt gcactgaact cgggatgttg gggattggag agagagaatt 1140
gocaaagtta cagcaaaaaa atctcttact tgcctttgtt tataaaaaa ttagttagatt 1200
ggaaaaacta gtgttaggga aagaatacac atgttcagag cctaatttcg taggaagggc 1260
ttttctctac cctgaaatga aggtaatcca aaggcatcca ttttctagag tttaaaagata 1320
tatttttgat atatttaagt atatttctca cactccagca ttaatatgtc tgtttaaaaa 1380
ttactaatc tcaaatggct caagaacatt agaatttaag taccttttag gtaattattt 1440
ttaagcaaat agcctggcag taagagattc tcatgccagc atgctttcat ttgtcagttg 1500
ttgtgactga gagataatga atgacacctg aaatgcata ttgtattttt ggagagttaa 1560
gggtataatt gaaggttggc agaccagttg ggcgtgattac tcttagagaa gaagaatgg 1620
aaaaatgaaa gaaggcagga aggaagaaa ggatatagga agagagggga gcagaaggca 1680
ggcatttttc tattttcccc acaaatattt tcaaaaaaaa tctgtatttt ctgggatatt 1740
tcattggcaa gaggaagaac tgggtgtttt aaagcagtat ggattcttta aatgcctctc 1800
cctgtacaaa gatagtaggc tttagataa taaactcaac cgtgtcaatt aacatttaaa 1860
ctggcatata gaaaaaaagg aggttttttc tgcattgtaa aataatcagt atggtttata 1920
tgttgaattt gacatttgtg tgaatttcca tgggtggccta gtgttttggt gcttctggta 1980
ttctgtaatt aagctcaact atttttttgt ggatttcaat ttttatcttc agaaagctca 2040
gacagtgaac ttctttaatg gtgggagttc agctcatgca tttctgatta tacaaaaaac 2100
tttgcagtag gttattttgc atttcagttt ttaactgaaa tcttagctaa acatttttac 2160
atgtaaatca ttgtatttac caaagattta aatcagttga ttaatttaatt aactcaaaa 2220
ctgtgaacta cttttaaaaa actagaaaaa agaaatgtta gtatctcaat tacaccaact 2280
gtgcaaatga actttgataa aatagaaaaa atctacattg gcctttgtga aatctgggga 2340
agagctttag gattctagta gatggatact gaatactcag gcccaactaa tttattaatg 2400
tatacatgtt gttttgtctt ttatgtctag tacagagaaa tgtgataatt ttttataata 2460
aatatttttt atgatgataa aag

```

2483

(2) INFORMATION ON SEQ ID NO. 82:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

ggtggtgggg gggggggtgt tgggccaaaa gacttcggta tctgacaaca gcatcatcta 60
cctcagtcac tagggtttct taataaaaaa gaggttggtat ttttgacttg gttattaagg120
ttattaaaaat tagcccttcc ttgaaatat gacatcagct ttgctgttct aaattttaaa180
ttagttgctt catcagtacc acacttccag ttctataacc aagccagttct cctcagtttt240
cccattagaa tggacatgtg ctgttcagcg tgtcatgtct gtaatgttcc atgcagagag300
tttggtcata gtattaaaga gaaaatacag tgaggtcaca atgtctccag agc      353

```

(2) INFORMATION ON SEQ ID NO. 83:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1039 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```

cggggataac caaacacagc tgtttacggt ttctccctta acccatgctt tcataaaccc 60
cttcgggacag cttcccggtc caggctttct aaccacacct accccagggg tgccgcattc 120
ctgcactcagc aagttctgagc cggctccctca aaaaacttga ttgtgccata aaaatcactg 180
gggatcttgtt taatacagct tctaactcaa tagatctggg agatcctgca tttctaacaa 240
gctcccgagt aaggcggagg ctgctgggtg gaggaccatg ctgtgagcag cagggcgaga 300

gtgccagggc ctgatatata ttgaaatat caccocctgaa gccatcgctg gccccacact 360
cctgtggact gatgccccag ggattcccac cccacttctg caaccccagc tatccttcac 420
tatccacccc atcccagact cccaccccag ggattgcccg tgaagacttt ggccagcaa 480
attgtgtctgg ttatgtgagt gttgttttaa tcagagatgt acatgattgc caatctgcat 540
ttcttacccg tgtgaccaca ctgttacgat gcaattctag ccaaaaaaaaa actttttcct 600
agtcttatg aaagcaata tacaatgatt ttcagtggc tcttggaata gaaacagtgg 660
tttgaagacc ccactgcccac ctttatggac tggcccccttt gactctgaat ccccgccctc 720
tgtcacctga gacccaaccc ctgactgggc caactccagt gaattccacc atttttcttc 780
ttcagaagcg ctttctctgtg tgagaccac atattttaac cttttgctcc tatccattt 840
ttaaagaatt agagaataaa ccaggccctg ttcttttccc ctgaaatccc tgcctctggc 900
ttcctaiaac catcatctaa ggtgacagag cagtgtctgg aataggcatc ttcctttcaa 960
ctttcccaaa actggccaca gataggctgg ccattgggaag ggtctttgga tttcggggga 1020
ggcaaacgtg ggggattgt
1039

```

(2) INFORMATION ON SEQ ID NO. 85:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 330 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```

agtgtattcca gcaaatgagg gtcagaaactt tcagttttatt gatggttatt cagccgcaga 60
tgagagttta tgcgtcagcc acttcaaattt ctgtaaacag aggcacaggg caaggactgt120
aaggggcaga actagtttttt cttcaaaattt gcctaggcat aataaggaaa atagcacttt180
tatttcaagg aaaccgattgg aatgtttcaa tgaggaagtt gttaatcaag ggcagtcgga240
tggatcaatg ggtaaatattt aggtggcgctc aaggaggggc ttatatccac tcaaaccgg300
atgttatttg gtcgggcccac gggttggaaagg 330

```

(2) INFORMATION ON SEQ ID NO. 86:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 235 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

atttaagtat tttttagttt ttaaaatgtc ttccgggtga gggaaggagc cccagccaga 60
aagcaattca atcatgggtca agtttccaac tgagtcactt tgtgagtggg taatcaggaa120
aaatgaggat ccaaaaagaca aaaatcaaa acagatggggg tctgtgactg gatctttatc180
atccattcta aatccgattg aatattgcgg gttacaaaa tgccaagggg gtgac 235

```

(2) INFORMATION ON SEQ ID NO. 88:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 866 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```

caggaccagc ctggccaaca tggcaaaacc ctgtctctac taaaaagtaa aaaaaattag 60
ccgggcatgg tggccttgctc ttgtagtcoc acttcagtcct aagtagctgg gactacaggc120
acgtgccaca agcccagcta atgtgggtgt ttgttagag atgaggtagg gccatattgc180
ccaggctcgt cttgaacacc ggggctcaag gaatctgccc atcttcgcct cccaaagtcc240
tgagatagca ggtgtgagtc atcatgcccc gccctcctga agttactaa caattgggat300
aactgagggg agagaagtga caattccact cagtctatta gaggtctgga tataaggtag360
ccacacaata actctaaact gactcttaac cattctatct tattgattg gaggcctgtct420
tctgccagat tttttgtggc ttgagatgat accttcgaac ccttctttca ctacctttct480
tacccttaat gtgccaaagt tgaacacagga tttgatctcc tgagctactt gttcgccttc540

tgctgcgtcac caagtaatct ggttcactct tcgtctcatt catgttattt tcaagtga600
caagacattt tgggggtcaa gtctctttgg gtgttttgtt tttatgtata taaaaattgga660
ttttgtgttc cctttccatg taagacccaa cttatatgga aactcacaat cataatgtaa720
agaagaagt aaagcctcgt gtattgtact tcaagatgcc tcctctgatg atagaaatctc780
cttgtaaaat aaataattgc attgtatctc agtcttccca tcaatattaa ttattaaata840
ttttagaatt ttttaatacc aactat                                     866

```

(2) INFORMATION ON SEQ ID NO. 90:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 846 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

ctccttgtcc aacggaaaaa acatggaagg gttaagccta aacaacccctc aaacggaact 60
ttatgccaga aaacaactac ggaataaaaa cccacaaaaa tacagagagg aacgttttta120
accttttaggg cotgcgtcct ctgccttttg cccatcaggg tcaaaagagta ggagtgagga180
aggaagggat gggacagcat cccctgggac gttcaagtac catccctggg ctccactctc240
cagccctaga gagtggacca gccagagcac ctcgctcggg ctctcagacc tgcctgcttg300
tctctaccaaa ccttggcagg gatctaggat ccatttagtg ggatcagggt ccagtcgaata360
ccattggggc tcaataaagt tcttagaacc acagagtcct gggccagggt cccaactcat420
aggtgacgga gttccctttc aagctcgtgc cgaattcggc acgagcgggc acgagcttga480
agggaactcc gtcagctatg agttgggacc ctggccctag actctgtggg tttaagaact540
tatttgagcc ccaatggtat tgactgggac ctgatccac taaatggatc ctagatccct600
gccaaagttg gtagagacaa agcagcaggt ctgagagtcc agacgaggtg ctctggctgg660
tccactctct aaggctggag aaggagacc aggatggtag ttgaacgtcc cagggatgct720
gtcccatccc ttcttctctc actcctactc tttagccctg atggccaaag ccagagacgc780
aggccctaaa ggtaaaaaac tcctctctgt attctctggc ttttactccc tagtgctctc840
gcataa                                     846

```

(2) INFORMATION ON SEQ ID NO. 92:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

cgaaagcgtc ggactaccgt tggtttccgc aacttctctg attatctctg ccaaggactt 60
tgcaataatat ttttccgcct tttctggaag gatttcgctg ctcccgaag gtcttggacg 120
agcgcctctag cctctgtggga aggttttggg ctctctgggt cggattttgc aatttctccc 180
tggggactgc cgtggagccg catccactgt ggattataat tgcaacatga cgcttgaaga 240
gctcgtggcg tgcgacaacg cggcgcagaa gatgcagacg gtgacgcgcg cgggtggagga 300
gcttttgggt gccgcctcag gccaggatcg cctcacagtg ggggtgtacg agtcggccaa 360
gttgatgaat ttggaccocag acagcgtggg cctctgcctc ttggccattg acgaggagga 420
ggaggatgac atcgccctgc aaatccactt cagcctcctc cagtcctctt gctgtgacaa 480
cgacatcaac atcgtgcggg tgtcgggcat gcagcgcctg gcgcagctcc ttggagagcc 540
ggcgcagacc cagggcacca cgcaggcccg agacctgc atgtctctg tccacgaacc 600
tcacacggac gccctggaaga gccacggctt ggtggagggt gccagctact gcgaagaaag 660
ccgggggcaac aaccagtggt tccctacat ctctcttcag gaacgctgag gcccttccca 720
cgagcagaat ctgttgagtt gctgccacaa acaaaaaata caataaatat ttgaaccccc 780
tcocccocag cacaaacccc ccaaaacaac ccaacccacg aggacctcg ggggcagagt 840
cgttgagac tgaggaggaa gagaggaggg agaaggggag tgagcgcccg cccccaggcg 900
agagatccag gagctggcgg cgcgcgatca gatggagaa gggggaccca gccagcagg 960
agacaggacc ccgaagctg aggccttggg atggagcaga agccggagtg gcggggcagc 1020
ctgccgcctt ccccatcacg gagggctcag actgtccact cgggggttga gtgagactga 1080
ctgcaagccc caccctcctt gagactggag ctggcgtctg catacgagag acttggttga 1140
acttggttgg tctctgtctg caccctcgag aagaccacac ttggggactt gggagctggg 1200
gtcgaagtgt cctgtgaccc atgaaactcc agtttgcgaa ttatagagac aatctatttt 1260
gttacttgca cttgttattc gaacctctga gagcgagatg ggaagcatag atatctatat 1320
ttttatttct actatgaggg ccttgtaata aatttctaaa gcctctgaaa aaaa 1374

```

(2) INFORMATION ON SEQ ID NO. 93:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 761 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

gacctgatggg ctggagccag actgtggtct gaggaggaga cacagcctta taagctgagg 60
gagtggagag gcccggggcc aggaagcag agacagacaa agcgtttaga gaagaagagal20
ggcagggaaag acaagccagg cacgatggcc accttccac cagcaaccag cgccccccag180
cagccccccag gcccgaggga cggaggactcc agcctggatg aatctgacct ctatagcctg240
gccccattcct acctcgggagg tggaggccgg aaaggtcgca ccaagagaga agctgctgcc300
aacaccaacc gccccagccc tggcggggcac gagaggaaac tggtagacaa gctgcagaat360
tcagagagga agaagcgagg ggcacgggcg tgagacagag ctggagatga ggccagacca420
tggacactac acccagcaat agagacggga ctgcggaggga aggaggaccc aggacaggat480
ccaggccggc ttgccacacc ccccacccct aggacttatt ccgctgact gagtctctga540
ggggctacca ggaagcgcc tccaacccta gcaaaagtgc aagatgggga gtgagagggt600
gggaatggag ggcagagcca ggaagatccc ccagaaaaaaga aagctacaga agaaactggg660
gctcctccag ggtggcagca acaataaata gacacgcacg gcagcacaaa aaaaaaaaaa720
aaaaaaaaatc ttgttaaaaa aaaaaaaaaa aaaaaaaaaa a

```

(2) INFORMATION ON SEQ ID NO. 94:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1825 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

agggaaagcta gtagcggacc ggaagtgagg caccctcggg ctccagacag cggcgacgtt 60
taaaagctgag cgacccaagt ccactggaga cggctcagctt ctccactcag gctcctccag 120
cccgaagccag aagacccccct cccccagaat tctggggggcc gatggaaagg agccgagtgca 180
gatcgcgagg taccacagag cgacagacgg gagcgacagg gagtggccag aagccccgcc 240
cctaggagtg atcggaagg ctcacccatc cgggtgagga acccgagga ccgctcccg 300

gcggaagcgc gaccatggct acgccccctg tggcgggtcc cgcagctcta cgcttcgccc 360
ccgcggctag ctggcaggtt gtgcgcggac gctgcgtgga acattttccg cgagtactgt 420
agtttctcg arctctgcgc gctgttgccc ctggcttggt tcgctaccgg caccacgaac 480
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gggccccagt cctgaaggcc ctgaatcacc actttccaga atctggacct atagtgcggg 600
atccccaggc tacaaggcag gatctgagga agattttgga gccacagga actttttacc 660
agcaggtgaa gcagctgtca gaggctcctg tggatttggc ctgaaagctg caggaaacttg 720
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gtcagctgga gaaagcactg cctacacocg aggcacagca gcttcaggat gtgctgagtt 840
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gacacttcaa tctggcccc ctaggccgac gaagagttca gtcccaatgg gctccaacta 1140
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caacccaggt catatctaag cctgagagca aggaagaaca tgcgatatac acagcagacc 1260
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gcttggtatt ctacatggac cccctgagac tatcattatt acctcctagg gccaggaagc 1440
cagtggttcc tcctctctg tgcagctcgg tcattacat aggggacttg gttttagact 1500
ctgatgagga agaaaaatggc caggggggaag gaaaggaatc tctggaaaaa tatcagaaga 1560
caaatgttga cactttgata cccactctct gtgaataacct acccccttct ggccacgggt 1620
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atgctctctg tactctagtc tcctgcctcc tcagctctgc aagtagttta gtaggaaatga 1740
agtggaaagc caggcttggga ttgcctaaact acactgctaa aaatatattg aatccttaat 1800
aattaaactt cggatttgtt aaaaaa
1825

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(2) INFORMATION ON SEQ ID NO. 95:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```

ccgggattcg ccctccgggg agcgattggt cctcggggagg ggcggggagg tggacgcggg 60
taccggcggt cgctcgggtcg gcagcctttg gtcagttggc agcggccaag gcgctgcggg 120
tcgggtggcg ccatgtcggt ctgcagcttc ttccggggcg aggtttttcca gaatacattt 180
gaacctggcg tttaactgtg tgccaagtgt ggcctatgagc tgttctccag ccgctcgaag 240
tatgcacact cgtctccatg gcccggcggtc accagagaca ttacgcgcga cagcgtggcc 300
aagcgtccgg agcacaatat atctgaagcc ttgaagggtg cctctggcga gtgtggcaat 360

gggttggggc acgagttcct gaacgacggc cccaagccgg gcgagtcggc attctgaata 420
ttcagcagct cgctgaagtt tgtccctaaa ggcaaagaaa cttctgcctc ccagggtcac 480
taggcgggca gccacacacc accccagacg gccaccacac tgaggccaca cgttggccat 540
tccaccttgg agttggaacc ctgggcgtcg agacaggaa ggcaggcgca gtggttgaaa 600
catcaggaca ctcaccaagg cccggctctg aacaagacct ttctgtttct tggaaaagag 660
actcatttgc tgatggttca tgcctttctg tgggacaggc ctgggctgtg cagccacact 720
gtcggctgag tttagccccc gctcactcta ggtgcctcca ggaggtgagc cctgggtgca 780
gctggtctct gaatgacgtt acaccctcac cttcttttcc tggccctgtc tctggactct 840
ccctgtgtag gcccaattcc aagacagact ctgctcctca ccgaagctta gcccacac 900
tcccaggctg cttaggagac agaattgaaa cggaggccgc ccctgccagc cgccttgccc 960
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ctgtgacctg ctgggaaggc aggcctgatg ggcacaccc tggcctctcg tccacgaggg 1080
gagaaacctc aacctgttct cacaatctgt gcggaagtag cttgcctcac ttctgcttag 1140
gaaaacggct gttgctccat aactctaac agcacaggc tgaggcctcg agtgacacac 1200
tgacgggagg ccttcccaaa ggtgtggtga ctgtgcctta ctgtacatgc tcggaggcct 1260
ggccatatag gaggggtggg gatgctgaaa tcacccccca tcttaagtga ttactttctg 1320
gagtaatcag gtggaatccc atagacaaat gaaacattca gatgtaaaaa aaaa 1374

```

(2) INFORMATION ON SEQ ID NO. 96:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2615 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

```

cttgggaagc  tctctggaatct  ttgtcaacct  gactgtgcga  ttctgtatct  tgggaaaaga  60
gtccttttat  gacacattcc  atactgtggc  tgacatgatg  tatttctgcc  agatgctggc  120
agtttgtgaa  actatcaatg  cagcaattgg  agtcactcag  tcaccgggtg  tgcctctctc  180
gatccagctt  ctgggaagaa  attttatttt  gtttatcatc  ttggcaccac  tgggaagaaa  240
gcagaaacaa  gctgtgggtt  tctttgtgtt  ttatttgttg  agtgcaattg  aaattttcag  300
gtactctttc  tacatgctga  cgtgcattga  catggattgg  aaggtgctca  catggcttcg  360
ttacactctg  tggattccct  tatatccact  gggatgtttg  gcggaagctg  tctcagtgat  420
tcagtccatt  ccaatatcca  atgagaccgg  acgattcagt  ttccatttgc  catatccagt  480
gaaaaacaaa  gtttagattt  ccttttttct  tcagatttat  cttataatga  tatttttagg  540
ttttatcata  aatttttctg  accctttata  acagcgcaga  cggcgctatg  gacaaaaaaa  600
gaaaaagatc  cactaaaaag  aaagattttg  atggcttctt  gccagtttga  gccataatctg  660
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attctcagtg  aggtctatct  ccttttcccc  agtaaacatt  ctgaattttc  tgtttatctta  780
ttgtagtact  tgcattgacat  ggtattctct  tatctgatga  gaggttcatt  cttgtgtatt  840
cagttaatga  caccaaaagg  ctacgcccac  cccaacccta  tctcatgttc  agtctgtcta  900

atcacatgcca  gagatttttt  tttcaaaaag  tgctttatcc  ctacaatgta  ctgacagcttc  960
ttacagttga  gatttgttct  tttcagctat  tgcttgtgaa  aaaaagcaag  actatgtcac1200
tctatagaag  gctgtttaaa  tgactcaggg  aggaatttaa  tattctgtac  ctaagggggt1080
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aagctgagat  gggaggatcc  tgagctcagg  aggtcaaggc  tgcatgtgag  cgagattgtg1620
ccactgcact  cgacgctcgg  gtgacagtgc  aagacctgtc  ctcaaaacaa  accaaaaccac1680
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aagggaacac  agtatgttag  tcaaaactgg  agtaaacagt  tacagccttt  gacaaaactg1800
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gtgggtggag  tgtatcattt  tgaatatgac  tcaaaaatac  ttcatctctg  tgcgtgtcag1980
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accaagtaaa  ataatgtttg  gagttaacact  tgcataaaag  aatttaagga  gtgataagtc2220
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tacttgtttg  tattgtattt  tgatatctct  gcagctgact  acgtgttaat  gggcagatca2460
gctttgcagt  agattatgct  gcatctcgtt  ggcaaaaatt  tgtattctta  gtgattgtta2520
caaacccctt  tattgtctgc  tgagaaagtg  aaagattgtg  tatttctatt  aaaacattta2580
caatcaaaaa  aaaaagaaa  aatagaagaa  aaagg

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(2) INFORMATION ON SEQ ID NO. 97:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 508 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

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gttggcagaa acccggtatc cgggtccggg gggcctccat cagcaagctc cagtgcctacg 60
tgtccctggc atttttagtg tcggttgggt aggcagtcac ggatcaggta atgcagtttgl20
ttgagccaag tcggcagttt gtaaaggact ccattcggct gggtaaaaa tgcactaaac180
ctgatagaaa agaattccag aagattgccg tggcaacagc aataggattt gctataatgg240
gattcattgg cttctttgtg aaattgatcc atattcctat taataacatc attgttgggt300
gctgaataca ttttgggaag gagtttttca tcttagagat tgggtgaacaa gtgtgaggggt360
gtgagaaact cacagaatac aaatttgcct gtatgttttg tgggtttttt tttttctctt420
caagatgttt tctatttcta aatttaaagta atttcaaagt aaaaaaaaaa aaaaagtcca480
cgcggccgcg aatttagtag tagtaggc

```

(2) INFORMATION ON SEQ ID NO. 98:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3588 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

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ctccgtctca aaaaaaaaaa aaaaaaaaaa aaaaaggaag ggaatcccat tttgtgatga 60
tttgggcaca ctacttgagc tgaggctagc agtcacatga ttttggctgt ctctgacctg 120
aagcttttga agtaaggtta tgtctcttcc ctgaagcttt gtttatagtg gtaatttggg 180
gagtttgagc tttgagcttg tcttagaaaa taagactgtc cacctgggga ggggagctta 240
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ttactatcta gaaggtggaa agaagtcatt gcttctgttc ctccagcagt cagttgacct 360
taggtttcct ttggtttata tcccagtttc ttaatactaa aacttatttg acttccatct 420
aggaagcaca caaaaaaaag gtcatttaaa accctggata taggctttaa aggatacaaa 480
aacagcagca tttgtctttt gccaggttca tcaccatttt gatgtgtcac ccatccttcc 540
accctccctt tctgtccccc aagcctccca gccaggccag atgtgaagat tctattaatc 600
actgtttcag agaaccattaa tcttctgata gaataattat ctactaaatt gcttattatc 660
tgtgactaac ttgcagagaa catctcaaca gtgcagtaaa atagctctcc tagacttgag 720
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agtcgtctct atctgagctt gcttttctga gcactttgtg gctgaatttg aaatggtaag 960
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aatcagttgt ccaagggata tctagctttg gttactcagt tctctgcagc taacagatat1140
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ctgaagactg tcaaacctggt cgataatcaa agaaaaaggtt ggttggttaga ataaagtaaaa1740
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tgtctcattt ttaagaggat ggcaaggtag acctcaaat agctcaacaa aactgggaat2700
ccaaggaatt gtgcttgttag ggaagagag gtgacttggg tgcctttaaac ccttggcac2760
cttgtcgggg ttataaaaaa aggaagctga gtaaaattgc ccttaccccc atcccaaatg2820
cgctccagga ttttagagct acccaacctg ttgtttatgt tgtgtgtt acattttgt2880
ttgttttggc gtttttcaaa atagccttgc ggtactgc atggaagatt caagcttttc2940
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tagtttctct gtttcccttt ctgagggtgg atgtctccag gcttcttcca cactctctc3120

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tcatgggtgc ggctggcagt acagtcaggc tgtggaggag ggctgagaag aaaggggcac3180
tgggtccagcc ccagggttttg tctgagacag gtacacagca gataccatcc cacccttcctc3240
tctaaagaac aggccagcca cacatataac cctttcccta ctttactaat gtatccctta3300
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tattacccgtt aaaacttgac caccocccata tcccaactcct ttttgtaaaa acaaatgctt3420
aaaactgtga gcttgccgtt cctttctatg tgttaatcag ttctcttcca tttgagctgt3480
gtggggaggga agggcattga aattgtaggt tgtaatcttg tgccaaccaa taaaaaccag3540
tatttcacac acaaaaaaaa aaaaaaaaaa aaaaaaaa 3588

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(2) INFORMATION ON SEQ ID NO. 99:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1218 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

tgggtggcgtt taaataacaa atctgctaaa gttaggcaac aggcagctga cttgatttct 60
cgaaactgctg tctgcatgaa gacttgtcaa gaggaataat tgatggggaca cttgggtgtt 120
gtattgtatg agtatctggg tgaagagtac cctgaagtat tgggcagcat tcttgggagca 180
ctgaaggcca ttgtaaatgt cataggtatg cataaagtga cccccaacta taaagatctg 240
ctgcctagac tcacccccat cttaaagaac agacatgaaa aagtacaaga gaattgtatt 300
gatcttgttg gtcgtattgc tgacagggga gctgaatatg tatctgcaag agagtggatg 360
aggattttgt ttgagctttt agagctctta aaagcccaaa aaaaggctat tcgtagagcc 420
acagccaaca catttgggta tattgcaaa gccaattggcc ctcatgatgt attggctaca 480
cttctgaaca acctcaaa gtcagaagaag cagaacagag ttgtaccac tttagcaata 540
gctattgttg cagaacaarg ttcacccctt acagtactcc ctgccttaat gaataaatc 600
agagttctgt aactgaatgt tcaaaatgga gtgttaaaat cgttttctct cttgtttgaa 660
tatattgttg aaatgggaaa agactacatt tatgcggtaa cacogttact tgaagatgct 720
cttggtgata gagaccttgt acacagacag acggctgatt cagtgtgaca gcacatgtca 780
tttgggtgtt atggaatttg ttgtgaagat tcgctgaatc acttgttgaa ctatgtatgg 840
cccaatgtgt ttgagacatc tctcatgtga attcaggcag ttatggggag cctagagggc 900
ctgagagttg ctattggacc atgtagaatg ttgcaatat gtttacaggg tcgttttcc 960
ccagcccgga aagtgcagga tgtatatgga aaaatttaca actccatcta cattggttcc 1020
caggacgctc tcatagcaca ttaccocaa atctacaacg atgataagaa ccacctaat 1080
atccgggtta tgaaccttgg cctatagctt agtaatttta agtgggttat tttgtgggtt 1140
aatgccactt gcttcacac tttaaactgc tttgagtttg tgggtgtacc tttaaacatg 1200
ca;atcagtg gtgactgg
1218

```

(2) INFORMATION ON SEQ ID NO. 100:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1303 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

gtgctcaaga agtgccttga gttgggtgac agtgccatgg ccagcaagaa tccagagatt 60
cagggttttat tacaaaaatgt aagtgggtcac ttggcgatttt tgtagtacat gcatgagtta 120
cctttttttct ctatgtctga gaactgtcag attaaaacaa gatggc aaaag agatcgttag 180
agtgcacaac aaaatcacta tcccattaga cacatcatca aaagcttatt tttattcttg 240
cactggaaga atcgtaagtc aactgtttct tgaccatggc agtgttcttg ctccaaatgg 300
tagtgactcc aaataatggt tctgttaaca ctttggcaga aaatgccagc tcagatatatt 360
tgagatacta aggattatct ttggacatgt actgcagctt cttgtctctg ttttggatta 420
ctggaatacc catgggacct ctcaagagtg ctggacttct aggacattaa gatgattgtc 480

agtcacattaa accttttcaat cccattatgc aatcttgttt gtaaatgtaa acctctaaaa 540
atatgggttaa taacattcaa cctgtttatt acaactttaa aggaacttca gtgaatttgt 600
ttttattttt taacaagatt tctgaaactga atatcatgaa ccatgttttg ataccctttt 660
ttcacgttgt gccaacggaa taggggtgtt gatattttct catatgttaa ggagatgctt 720
caaaaatgtca attgtcttaa acttaaatca cctctcaaga gaccaaggta catttaccct 780
attgtgtata taatgttttaa tatttgtcag agcattctcc aggtttgcag ttttatttct 840
ataaagtatg ggtattatgt tgctcagtta ctcaaatggt actgtattgt ttatatattg 900
accocaaata acatcgtctg tactttctgt tttctgtatt gtatttgtgc aggtattctt 960
aggctttatc agtgtaatct ctgcctttta agatatgtac agaaaatgtc catataaatt 1020
tccattgaag tcgaatgata ctgagaagcc tgtaaaagg agaaaaaaac ataaagctgt 1080
tttcccatata agttttttta aattgtatat tgtatttcta gtaattctcc aaaagaatgt 1140
aaaataggaaa tagaagagtg atgcttatgt taagtccata cactacagta gaagaatgga 1200
agcagtgcaa ataaattaca tttttcccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaagt 1260
atacgttgga atgaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1303

```

(2) INFORMATION ON SEQ ID NO. 101:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2333 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

tgaaaatgac ggacagtata ttccagaaagg ctatttccaaag ctcaagatat ataattgtga 60
actagaaaaat gtacagaaat ttgaggggcct gacagacattc tcagatacgt tcaagttgtta 120
ccgaggcaag tcggatgaaa atgaagatccc ttctgtggtt ggagagttta agggctccct 180
tcggatctcac cctctgccgg atgacccagc cgtgccagcc cctcccagac agtttcggga 240
attacctgac agcgtccccc aggaatgcac ggttaggatt tacattgttc gaggcttaga 300
gctccagccc caggacaaca atggcctgtg tgacccttac ataaaaataa cactgggcaa 360
aaaaagtcatt gaagaccgag atcaactcat tcccaacact ctcaaacccag tctttggcag 420
gatgtacgaa ctgagctgct acttacctca agaaaaagac ctgaaaattt ctgtctatga 480
ttatgacacc tttaccgggg atgaaaaagt aggagaaaca attattgtac tggaaaaaccg 540
attcctttcc cgctttgggt cccactgcgg cataccagag gagtactgtg tttctggagt 600
caatacctgg cgagatcaac tgagaccac acagctgctt caaaatgtcg ccagattcaa 660
aggcttcccc caaccatccc tttccgaaga tgggagtaga atcagatagt gaggacgaga 720
ctacagcttg gatgaattg aagccaaaca aatcctgcac cagcacctcg gggccctga 780
agagcggctg gctcttcaca tcttcaggac tcaggggctg gtccctgagc agctggaaaac 840
aaggactttg cacagacccc tccagcccaa catttcccag ggaaaaacttc agatgtgggt 900
ggatgttttc cccaagattt tggggccccc agggccctcct ttcaaacatca caccocggaa 960
agccaagaaa tactacctgc gtgtgatcat ctggaacacc aaggacgtta tcttggacga1020

gaaaagcattc acaggagagg aaatgagtga catctacgtc aaaggcctgga ttcctggcaa1080
tgaagaaaaa aaacagaaaa cagatgtcca ttacagatct ttggatgggt aagggaaatt1140
taactggcga tttgttttcc cgtttgacta ccttccagcc gaacaaactct gtatcgttgc1200
gaaaaaaagg catttctgga gtattgacca aacggaattt cgaatccccc ccaggctgat1260
cattccagata tgggacaaatg acaagtttct tctggatgac tacttggggt tcttagaact1320
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tccggacccc aaagccatga acccccctaa agccaaagaca gccctccctct ttgagcagaa1440
gtccatgaaa ggaatggtggc catgctacgc agagaaaagt ggccggccgg taatggctgag1500
gaaagtggag atgacattgg aaatcctcaa cgagaaggag gccgacgaga ggccagccgg1560
gaaggggcgg gacgaaccca acatgaacccc aagctgggac ttaccaaatc gaccagaac1620
ctccttctct tgggttcaaca acccatgcaa gaccatgaag ttcatcgtgt ggcggcgtt1680
taagtgggct atcatcggtc tgcctgttct gcttatcctg ctgctctctg tggccgtgct1740
ccctcactat ttggcgaact atttgtcaat gaagattgta aagccaaagt ttgaacaaag1800
gcaaaaggctt catttccaaga gtcatccagc aatgagagaa tctctgctctc atgagccaa1860
atccagtggt attttctgtc tgagaccaca cccagctagc aggtttacgc atgtcacccga1920
gccccattga tttcccagag gtcttagtcc tggaaaagta ggcccaacaa caacgtttgc1980
atcatgttat ctcttaagta ttaaaagttt tatttttaac agtttttca2040
aaaaattttt caagtggtgct ggttccattt aaaaatcatc tttttatatt tgccttcgggt2100
cttagacttc agcttttggg aattgctaaa tagaattcaa aaatctctgc atcctgaggt2160
gatatacttc atatttgtta tcaactgaaa gagctgtgca ttataaaatc agttagaata2220
gttagaocaa ttcttattta tgcccacaac cattgtcata ttttgtatgg atgtcataaa2280
agtctatatta acctctgtaa tgaaactaaa taaaaatgct tcacctttaa aac 2333

```

(2) INFORMATION ON SEQ ID NO. 102:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1377 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

cattactgtt atatgagaaa catttttagta atttaataaa aggataatgt ttatttataaa 60
aacctgacct ttccagagta attttgtttt gcacattcat gtttattgaa gtggactaat 120
ttctataatg caaatcagag ttaaatatta aaaatttgtt aaatacaatt gacataggaa 180
ttacattaaa atattaggaa gaaacaagga caaattttaga ccttgaatcc gaagagataa 240
agccttacct ccttttcaaat ggagagatga tgaaaaccca ctcatcagtt ctttcagaac 300
aaaaagacag tcactgtgata agagtatgac atggatgaaa tgccttcacag gggccttgga 360
catctttaat ttctgcatg atgtgaaaga ggtggacttt acagataatg gacgagaagc 420
caacattagt aaaaaggaatc ccaacttctct cccatagaat tagaaacatg tgaagtaca 480
ataaacttct tgttcaaatc accagcatca gagagcttcc catttgcacg tagaccttga 540

atttatattt attgacaaag ttctaatttg tatgtatatt ttgtgcatat tcaccaataa 600
cagttataat taattatgtg ttatagttaa tatatgcacc taccttcttc cgttagtgtg 660
tcagtataat gtgtattttg tcattttttc aaagagagtg ttgtagggtt tccctgtagt 720
tcttccttta tagcttttct tctgataacc atgacttcag gagcttttaa atcatctatc 780
ttgcatttgt gtctggcgga gaactagcca tcagcctcct gaagcctgcc atcattgtta 840
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tgggtggcac tggattccac ccaactgcca agttagtatt gtttagagatt tcattttaca 960
acacaaaaat aagcctgtgt caaagatttt aaaatcoatg aaagttaaaa tctagaaaagal 1020
ccttagagaa ccagcccaacc aactctctca tttttaaagt gaaggattca tagcacagat 1080
tacttgccca agatcatcca ggaacgaaga caagaatcca aatgtacttg gggacaagaal 1140
ttagtcccca aattcagtggt tcttctcagt attaaacatt gcccctttcg acaaattttg 1200
gatttcaatc ttggtatatt tcagtataacc tgctgattta ttaggttact gggtagatga 1260
cattagaatg tagatagcgt gcacgcctatg atagactctg ctaagacatg ttcccagtg 1320
ccagcagcaa tgtagatatg tgtgacagtg gtcattgtaga agttataaag cagagta 1377

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(2) INFORMATION ON SEQ ID NO. 103:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

ataaggaatg agaagaaagg ctgtgtctta tcagtaggtg agatggaact ggtcctggta 60
gtgttgagac aggacaggca cttagtctctg atgctgtggt cctttgtgat agtagagcac120
cggggttaac caccactcct ttaggctact tgtagtgaca acagaagtaa aatatttcaal80
ttatttaatt tagaatgtta tgttttactg gaacctgcaa tatgcatgta cagaattaat240
aatttttact ctttttggtca agttatacta aggcaaaagg agtggattca aaagtgagac300
attgacaggc cattt                                     315

```

(2) INFORMATION ON SEQ ID NO. 104:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2355 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

atgatcatgc cactgcactc catcctgggt gacagcaaga tcttgtaaaa aaaaaaaaaa 60
aaaaaaaaac gagtgaaaaa ggaagtaga aggcagctgc tggcctagat gttgggttgg 120
gaatattagg tgatccctgt gagattctgg atccagagca attctcttag ctcttgactt 180
tgccaaagtg tagatagcct ttatccagca gtatttttaa tgggggaatgc aacgtgaggg 240
caactgaaca attccccccg tggctgcccc gatagtcaca gtcaaggttg gtaggtctccc 300
ttccagccag tgacctaccc aaaccttttg ttctgtaaaa ctgctctgga aataccggga 360
agccccagtt tctcacgtgg ttcttagctt ctccagactc agcccaaat aggaagtcca 420
gaagcacatg atgggtgaaaa acctaggatt tggcagcctt ccagaatggt atggaatctg 480
aggggaagatt tatgttttgt tttggaggat agctcaagtt gaattttctt tccagccagt 540
taccttttca acctacccat acctgttaca actcttacac aaatacttag atatttatta 600
gatagccctg aattcaactct aattataaac agggagtgtg aactgcccc agatgttctt 660
gggtcgggta aaagcagctg gagtgaagca ctcatcttcc ataaaggtaa caaagggcag 720
ctcagtggtt actcaagctc aaaaggggtt ttttaagagc aagcattggt taagtctgtg 780
tatactgagt tgggaagtgt ttcagcacat tcttttttag tggagtgaia gttctgaagc 840
ccccctttta ctctctcttg gtttttcatt ataattggta gccatctcat gaactgtctc 900
tgactgttgt ctctttgttg tcatgtgatt gtgagcttgc tttctgactt gcatttctga 960
ctttatcctg ttgttaggaa gatagaaact aggttttgaa agatctacat attcaagcga1020
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ttatgaaga acaatatagt ctgggaatcc cagaaatgtc agccaaaggt ctaagaagtc1140
atctctctca aatactttta taaagaagta tttcgaggag atactgtgcc aaaaaggtt1200
gactggctcc cagattccag ttatttttaa aaagcaactt accactaaat ccttgagtct1260
ccatagagta acagttaaag aactgatgta acagactctc ctctcaaaag atctctctg1320
gaagagacta tcagcggcag cattctccag ggaagacca tccccagtg ccagagcttg1380
cactcctggag actaaagatt gcaacttttt gtatgttttt gtccaaatgc aatccccatt1440
ctgtgcctct tagcatgcag tttagatttg acaaaacaaga ttcttaagga atgactttat1500
taactataac atgggtcacg ctattatata aatatatat ctggtctatg ttctaataatg1560
gagatgttgt gtgcaatgct ggccgtgggt ggtctgtgta atgctttaac ttgtatggag1620
gagggccagg tcagagctga gatgtggcct gaacctctcc tgatctgac cttaatttta1680
gaactgtcaa gatgtcactt tctccccctc tgccttttag tggatctgta catatactca1740
aaacagtaat tctctgggtc catcatcaac tgctaattct gtatttataa agaattttca1800
gatggacatg tacaaaattt aactcaaac atccccagtc cagatcacgg gcagcgtgta1860
ggtgaccaca ccagagcctc agcctcgggtc ctcttcagcc gtccgggatg gatccaggca1920
tttctcttaa atctcagagg tagcagtaaa cttttcagta ttgctgttag caagtgtgtg1980
tttgccaata gatcacctat atactaatgt gccaaagtaaa tggctctgtc acatctgtct2040
ccactgttgt cccacgggtg ccatgaagtg tgtgaggagc cctctcatct gagggatgag2100
tgctgcgttg actacgtcta tcaggattgt gttgtgtgga atattctatc acataaattt2160
tatatgcaca gtaatttccc tttttatag tcaagtaact atttgtaaaa gttatactca2220
caaattatta taatgattac taatatattt ttccatggtt tcatctgctg aataaaact2280
gtttacacct gttaaaaaaa aaaaagttaa aaggaggagg tgggaaaaaa aagctggggg2340
ggggggccgg tagcc
2355

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(2) INFORMATION ON SEQ ID NO. 105:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1339 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

attcggcacg agcatgaaac atgctcattt tacctaacag taaacaagta tgttttgata 60
gatatctggt aatatgccta tagtggaag aaatggactt gaggctccag gagatttcat 120
tttattcacc ctggtcagat acaataaagg ctatgagtat aaatacataa ctccctaacc 180
agggtgtagg catgttcgat aatatcaaat cttttgatgc tggacccaag agaggaaaag 240
ttgtagctaa atgttgattt acttataact agacgtctat gtgagaaaaa atagtgtatac 300
atataatga tatgcagaag tcaacttttt tatcaggctt tattctcctt acaaagccac 360
agtttaaact tctgcaaacag ttggtttatg ttaatgatag acaaataccg agtgttttgt 420
actttttcca actaccactg taatgataat cttttctcac tatatacatg caactctctg 480
gcttcatttc catgaagctg ttccaataata ttcaagtatac ttgtctctta atgctgtctc 540
tgttaacagt gatctctttc tttttttcat tcttatatct tcattagttc atcataaatc 600
tgtccagttg aggcctcagg accacggcat gatctcatga ctccgaagta ttttacagaa 660
acatttttta aataaggaaa atattttata taccagatgg ttccacaagt atggctcata 720
gctagttttt tttttctctc taaaaaatgt cagggtttttt aaatcattta ccttattaaa 780
atgaaaaagt ccataacttaa cttttaaagg aaagacctga cttgtctttt ctctatttag 840
actgtttttt tactttacta atcttttaaac tatcaggaaa aaaacccaaa ctttatacca 900
atgatttagt aattttgagg catagggtag cttacgtagt ggaggatgtg ccaaatattc 960
tcttcaaatg ccaccttctc aatttataac taaaatagtg ttatctgact aattcctctg 1020
aattttgatg taagatctat ataggccccc aaaatgatcg tagtacatgc cagtcatctc 1080
tcagtgaaat aaatacaata ccagagtaca ttatgggttt tattgctttc ttttatggta 1140
gacctgttaa tggggaaaaa atacatcaaa tcaaatagaa tcttatatct gtatgtttaa 1200
atagagcact tacctgaagt cagtggcctg gatcatagcc ctggatcatt tccacgtctg 1260
tcctgtgctg ggtggacctt ggacaaggcg ctgcagtagg tgatggctga gagcccttcc 1320
ctgttcccaa gtgccttgt

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(2) INFORMATION ON SEQ ID NO. 106:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3751 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

gatcgcgagc ggccctttgga atctattgtg caaaagaagt ttcatatttg ttacttagac 60
ctaaagatcac ttattaaaaa tctctatttt ccccaagccc agcaaacggt gactctctgg 120
caaacctgaa aaacctgaaa tgccactttc atgcagtttg tttgaagtta agtgggaatc 180
tttcaaatga cgaagctgac agaactcagc accaagggtc cgttatctgt agtatgctgt 240
aaaatggaa attttttaaa gaaggcaaat aagtacttaa aagtgcagctg agcaataaaa 300
tgggtccaata ataggttaaa gcaacagaaa cagaaggaga cctggttgct ttatgccttt 360
acctttacat ggaaataaaa cccaatgcac atcttatgta aaccataaag gaagggaaat 420
aaacctctgt atgtctccat ctgtcgaggtg tccctttggt atctctgtga gacagagaag 480
ctcattttgt tttgttttca gcatctttct ctgatgtacg tttttaagga ttttgtaaat 540
gctgttttca gtgttttaaa tagtgctatt tttccttggt tttaaaaaat aatctctgac 600
tgtattctac tatgtccata cagatgttac aaatcgacag ttttattctt agactcagt 660
gatccaaagt gtataacca tatataacca ttttacctga atcatttagt tttttaattc 720
atttactaat gctataaaa ttcttatatt accccaagta ttgcatcag ctggtttata 780
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tgggaagta aaatgtacct catatacaaa ttaggcgaaa ttgaagcaga 1080
aatctaggaa gtgtgtgctt ctgttatgtt gagttttgct tcagactaac taatgcatac 1140
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tgtgtcagag atttctctac ccocttatgt attttgttag atttgtcaac aggaagcaca 1260
tgattcgaaa catcttggga cagaccaaaa ccaactgacag atggcaagct tggcgagct 1320
tgatttccct tctcaaatct gctcaactcc aagagttctg agaaaactgt aaaaatttgc 1380
ctctgtcact caagttctac aaatgttato ttgataaact ttcaggtgaa ctatttccat 1440
gtctgtgata taggcatctt attcactgca cctgtgcaca cccagcacc cccgccccgc 1500
acattatttg aaagactgg aaattcaatg ttagggaacag taaactctat tctttttcca 1560
gggagcagctg tccctctaaa agttaaaagt aatcaagaaa aactgtctat ttttagccta 1620
aagtaaaagg ttggaagaaa attcatttta cattgggtag acagtaaaaa acaagtaaaa 1680
taacttgaca tggagcactt tagatccctt cccctccatg ggctttggag cacaagatga 1740
acctttgagc cctgtaaaag ggattgtaat ttctataaag ctgtaaatg tggaggtatg 1800
tgggttccat tgaattgacc ctocaaagat accattcaaa taacctggga gaatgcatac 1860
aattattcag ataaattaaa ctgcatgaat ctgattcaga ggcattgca tcatattgt 1920
gcccttaata ccaatttgat atcataaata caagtgaatg caattggaat tttagtaaca 1980
aaccttaatt ttaaaaagg gttagacaaat gttggttaaa aaaaaaaa aacagttacc 2040
aggttctctg tgtttgcacc aagtaattga catgttttt gtttaataca tgtggaccat 2100
gaacagtat catctacttt tttcaaatga tatgtgttag aaaaattctc tgaagaagt 2160
gagattttaa aatttttccc tttcaatgtt gttttaatgt tatttcttat tttgtttttt 2220
tgattgatag cacagtgtata aatcataata ctgacaaaaa tctctctctc tctcaaaaa 2280
gagccatata tatgtctgta tatatgggac ctactgcttc tctgaggaaa tgcataactc 2340
gttaatatca gacaaaaatga gcaatttgga gtgctcataa tatattccaa ttttttttgg 2400
aattttcgat ggaattgtat ttcaataaag ccatgcaagg tgaaaacttt ataaactttt 2460
accttcaag ttagggttaa ttctgatcca attttctgt cattttgtga cctcccaatg 2520
caaatgtcta aattacaatg cagacattaa gaaaagaagt tgactggagg ggttgaattc 2580

cttgagaatt tattttatag tctaaatcac aaatacttta ctcaatttag ttttaaaat 2640
agtaaaactga atatttttgt tgaagaacct caagagtcda tcttctgttt ggaattgttt 2700
tctctgtttt ccttactata aatcatttaa aaactgaaat catttcttta gatggcaaa 2760
gtctgtctct tgagaaaaaa gtaaaaactc cctattttca gtatctgtag caactgaaa 2820
aggctcttgt atagccagaa acaagttatg ttgaagttag cttttctttg tcaacagttt 2880
tggcacaata aactctgaaa gtattaaacac ttgattttct actggggccc ttcaagctgt 2940
gtttggaagaa atttcaaccag attatctaca tttagagtata atcatgtgtg ttgaagagat 3000
ggactaggtta atcaagattt gttgtcactt aaattttttt tgattttttt ccaagccagt 3060
tttttttaaa tctaaaatgt ttttgaggta tgggtacatt aattgtaatg taaactattc 3120
tacaactgtt ttttgcagct tataggcagg taaattttgc tattactatt gaatacaaa 3180
gacaattctat ttatgcacc tcaaacagcg tttagtaacaa ttttagtgac aaggtataaa 3240
acatccatct ggaattgttaa tttgaagatg taaatttatc gtgttttaaa tttttccagg 3300
catctgaaaa ccttatctgc tagacaatgt aagattcaaa cagagtttat tgggattctg 3360
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tattgaaaaa agatgcagtc aaagtctttt cagacatgac caaacctgga gaattctctc 3540
aacccatcaa tgcctataag atttttgttc ttctgtttca caaccagtgt tataacagaa 3600
ataactagcta ctgtttttct tctgtgtgtg gaagtaatga atctgtattt atgtgactgt 3660
ttatgtattc aattaaacac taagaataaa aacatttcaat cctttaatta ataaaaaaa 3720
aaaaaataaa aaaaaaataa aaaaaaataa a

```

(2) INFORMATION ON SEQ ID NO. 107:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```
cgctcggccc ccgaggagag atcgaggtgt acttggccaa gactctggcg gaaaagctgt 60
atctatgtca gtaccctgtg cgtccagcct cgatgacctt cgatgacctt ccgcacctct120
cagccaagat caagcccaag cagcagaagg tagagcttga gatggccatt gacacctga180
accccaacta ttgcccgcagc aaaggggagc agattgcgct gaacgtggac ggggcctgcg240
ccgacgagac cagcacgtat tcctcgaagc tgatggacaa gcagaccttc tgcctctccc300
```

(2) INFORMATION ON SEQ ID NO. 108:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1465 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

```

gccaaccttc cctcccccaa ccttgggggc gccccagggt tctgtggcac tgcctgttcc 60
tctctgggtg cactggcagc cctgtccttc ctaggaggac tggaaacctaa ttctcctgag 120
gctgagggag ggtggagggt ctcaaaggcaa cgcctggccc acgacggagt gccaggagca 180
ctaacagctac ccttagcttg ctttcctcct ccctcctttt tattttcaag ttctctttta 240
ttctcctctg cgtaaacaacc ttcttccctt ctgcaccact gcccgtaacc ttaccocgcc 300
cgccacctcc ttgctacccc actcttgaaa ccacagctgt tggcagggttc cccagctcat 360
gccagcctca tctcctttct tgcctagccc caaaggccct ccaggcaaca tggggggccc 420
agtcagagag ccggcactct cagttgccct ctggttgagt tggggggcag ctctgggggc 480
cgtggcttgt gccatggctc tgcctgaccca acaaacagag ctgcagagcc tcaggagaga 540
ggtgagccgg ctgcaggggg caggaggccc ctcccagaat ggggaagggt atccctggca 600
gagtcctccc gagcagagtt ccgatgccct ggaagcctgg gagagtgggg agagatcccc 660
gaaaaggaga gcagtgctca cccaaaaaca gaagaagcag cactctgtcc tgcacctggg 720
tcccattaac gccacctcca aggatgactc cgatgtgaca gagggtgatg gccaaccagg 780
tcttaggcgt gggagaggcc tacaggccca aggatattgt gtccgaatcc aggatgctgg 840
agtttatctg ctgtatagcc aggtcctggt tcaagacgtg actttcacca tgggtcaggt 900
ggtgtctcga gaaggccaag gaaggcagga gactctattc cgatgtataa gaagtatgcc 960
ctcccaccgg gaccgggccc acaacagctg ctatagcgca ggtgtcttcc atttacacca 1020
aggggatatt ctgagtgtca taattccccc ggcaaggggc aaacttaacc tctctccaca 1080
tggaaacctc ctgggggttg tgaaactgtg attgtgttat aaaaagtggc tcccagcttg 1140
gaagaccagg ggggtacat actggagaca gccaaagact gagtataata aggagagggg 1200
atgtgcagga acagaggcgt ctctcctgggt ttggctcccc gttcctcact ttctcctttt 1260
cattcccaac ccttagactt tgatttttac gatattctgc ttctgttccc catggagctc 1320
cgaattcttg cgtgtgtgta gatgaggggc gggggacggg cgccaggcat tgttcagacc 1380
tggtcggggc ccactggaag catccagaac agcaccacca tctaacggcc gctcagggga 1440
agcaccggcg ggtttgggcg aagtc

```

(2) INFORMATION ON SEQ ID NO. 109:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1488 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

```

cgggcggagg agcaggatgg agatccctgt gcctgtgcag ccgtcttggc tgcgcccgcg 60
ctcggccccc ttgcccggag ttctgggcgc cggacgcctc ttgaccagc gcttcggcga 120
ggggctgctg gaggccgagc tggtcgcgct ctgccccacc acgctcgccc cctactacct 180
gcgcgcaccc agcgtggcgc tgcctgtggc ccagggtgcc acggaccccc gccacttttc 240
ggtgctgcta gacgtgaagc acttctcgcc ggaggaaatt gctgtcaagg ttgtggggcg 300
acacgtggag gtgcacgcgc gccacgagga gcgccggat gagcacggat tcgtcgcgcg 360
cgagttccac cgtcgtacc gcctgcccgc tggcgtggat ccggctcgcc tgacgtccgc 420
gctgtccccc gagggcgtcc tgtccatcca gccgcacca gcgtcggccc agggcccacc 480
gccagccgca gccaaagtag agggggctgg gccgcgccc gcccccggga gccctccacc 540
gctccctcta ttaaaaggca tctgactccg ccagccaga tgtcccgagt gcgccaagga 600
ctgtcccttc acccactcct ggattctgcc ctgacctcca tcctggacac tgccttgata 660
acatagaccc ttccactgac accctcgctc tcagagcccc tccagctttc cgaccccaca 720
ccgacaactc ccgggcttcc agaccctacc agcactacc taacctcag ccgacagtct 780
cagccccacc gaccacttt ctgtgcatat agccccactt aagaccctc ctctacttcc 840
ttctgagtc ttacaaaaga catccgggta ctacatttcc atcccttccc tattttgaca 900
cgaattatag gtgtagacag ccttgcccca accccaggcc agtcaggcac aatcccccca 960
cccccaaac gtccctggact gccacagact cccactccag accatccagg cctggttccc1020
aagaccgat ccttccctgc caaccagaca gtctacaact gcccccctca gcccattttc1080
tgccgtgaaa cccacgcccag ccacaccaga ctctggaacc ctttttcgac tgcccacaact1140
cttggaacc aggccaaacta gaacacccaa caccaaactg tacagactct cccaccccaal1200
cctccccaaga cctctgcacg atgtcctagg cccctcccc aactcctaacc agaccccctc1260
ccctaaagtc cctttgtctt gaaccccagg tcttcaacca gatctcctg gcaacccacc1320
tcccaccctc cctctcttct ccttcaagac ccaactgagc acccgctctg attccccaca1380
gcctttctcc ctgccaccac tcccttagtc ttctccaggc ttactctccc aataaatgtg1440
ctagagctct gccaaaaaaa agaaaaaaa gtcgacgcgg ccggaatt 1488

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(2) INFORMATION ON SEQ ID NO. 110:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 783 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

aacatatgtt tgaaggtaa tttgagagaa atatgaagaa ctgaggagga aaaaaaaaaa 60
aaagaaaaga accaacaacc tcaactgcct actccaaaat gttgggtcatt ttatgttaag120
ggaagaattc cagggtatgg ccatggagtg tacaagtatg tgggcagatt ttcagcaaac180
tcctttccca ctgtttaagg agttagtggg ttactgccat tcaactcata atccagtagg240
atccagtgat cottacaagt tagaaaaacat aatcttctgc cttctcatga tccaaactaa300
gccttactct tcttgaaatt ttaacctatg atattttctg tgcctgaata tttgttatgt360
agataacaag accctcagtg cttcctgttt ttacacatttt ccttttcaaa tagggctctaa420
ctcagcaact cgcttttaggt cagcagcctc cctgaagacc aaaattagaa tatccatgac480
ctagttttcc atcgctgttt ctgactctga gctacagagt ctggtgaagc tcaactctgg540
gcttcatctg gcaacatctt tatccgtagt ggggtatggt gacactagcc caatgaaatg600
aattaaagtg gaccatagg gctgagctct ctgtgggctg gcagtcctgg aagccagctt660
tcctcgcttc tcatcaactg aatgaggtca gcattgtctat tcagcttctg ttatttttca720
agaataatca cgctttcctg aatccaaact aatccatcac cggggggtggg ttttaagtgg780
gct

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783

(2) INFORMATION ON SEQ ID NO. 111:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1045 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

tcgtgtctgt ggacaactgt tactgttctt ccgtggccaa ccattggcgc caccagccct 60
accoccgctc cggccacttt cctggacag tgccctcgca ggagtactca caccogctcc 120
cgccacacac ctcgctcccc cagtcccttc ccagcctggc ggtcagagac tggcctgacg 180
cctcccagca gcccgggccac caggatttct acagggtgta tgggcagccg tccacccaaac 240

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actacgtgac gagctaacgc cagcgaggcg gcgggcgctt ggggaatctt cctccccagc 300
ccccgggctc gggagttatg catccagaga cctggccctc taccttcttc gccctccccc 360
ttcctcatto cattgccccga ggtcttttcc ttttggtatt tgttttgggt ttggctttgt 420
ttttgatttt tttttattat gaattctctg gacgcagagg tgacagtggg agctggcctg 480
ggccaggagc ggcaggtggc ctggagatgg gaaagtgtct gtgtcgaggc gctgagctct 540
ctctctgttt ctctcttttt cctctactcc ttccccctca cccccccgtg gctggaagga 600
acctcggtct cctgaaaagc ttgggggtcc cacccttctt accccacccg ggaggaaagc 660
ccaggggccc gggctgtttt ctctctttgt tttcttttgg ggcagtttga tcaactgatc 720
agtaaggaat gaccttttaga ttgtgcgact ttgtgttttg ttttttttaa tttttttaaa 780
ccaagaatga tttctctgc ttctctctcc tcaccatctt cccagacagga gttcaaaaggc 840
cactttctca gacgtttttg gcaacttccg cctcagagtg gaattcttta aagacaggagc 900
ccctatgtcc aggaaggagg aaaaggaact ttgccaatga tagtgaccac agcaaaagca 960
aataataata atattataaa taataaaaag gaaaaaaaat aatagaataa aaacccaatal 1020
gcacagcccc ttgttggaag tccag                                     1045

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(2) INFORMATION ON SEQ ID NO. 112:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1386 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

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cacactcact gcccatgaag gaagaggggg caagtgtacc gaggaagggg atgcctcaca 60
gcaagagggc tgcaccttag gttctgacct catctgcctc agtgagagcc aggtttctga 120
ggaacaagaa gagatggggg ggcacagcag cgcggcccca gccacggcca gtgtgaatgc 180
agaggagatc aggatagccc gtattcatga gtgtcagttg gtgggtggag atgtcccaaa 240
ccgggatgtc ctgtctgcac acaagatga cgtgaaggag gagaagggtg gtcagggaag 300
tttcccagag ctgcccctcag aggagtgaaa gggacaattt ggctgaagtc tttctctgaa 360
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ttttaagtat tttcttaatt tgaataataa aaccagagga aatgcataca gggcatgagc 480
aacctgagga aaccttttgt gacatgaatt gttctacgat gaatttttgc tttagtattt 540
taataaagat tacaagaaca atggcctact tggggtgaga gggagctgag gatgtctgag 600
gagggaatag tattgcaggg aagactgaga aaacagttag atgacagttt tgagtatact 660
ctgcactttt caatttgtga atctttcttg gcacttttag gctttttaat tttgtttgag 720
aatgcaaatg tatactgtaa gtctactctt actatctact atgcccactt caccatctct 780
taaggactcg gcaattgtcc acagtccagc tgcagaagag ggtaggtctat gaacagtcac 840
ccgtgtctgc tgtagccccc acagaggcaa tcatgcccaa tagattcaag agaagctaa 900
cggaatgga ggggtggaag tgtgatctgt gggagctgtc gggctgttta ctcatctgc 960
tatcaatttc ttattaatca atcttgatga ttcttattaa ttaatcacat ttgcaggaaal 1020

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ttcagatgag gcaagaaaaa ttatttggcc tgggttaagac tgaagaagcatt ccaaatagg1080
cttagactgt gcaaggggct tagctaagtt atcgagctta aaacccgccta attaaacaa1140
cattatttga acagttaact catgccacgc actgtgttgg gcttagtaat aaaaaaaag1200
aaagataaag gctttgtcta gcataaata aaaggctccaa ggaattttaa tctggaagag1260
aacatattgc aattttttaa ctatgcacgc tttttttttc tttttccatt caaataggc1320
cgggttcagc cccagaaggg cacaaaatga atgaataaat aaataaatga ataaagacaal380
aaaaaa                                     1386

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(2) INFORMATION ON SEQ ID NO. 113:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1747 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

ccagctctgtg agcccttgtc ctgtgggtcc ccacogtctg tcgccaatgc agtggcaact 60
ggagaggcac acacctatga aagtgaagtg aaactcagat gtctggaagg ttatacgaatg 120
gatacagata cagatacatt caccctgtcag aaagatggtc gctgggtccc tgagagaatc 180
tcctgcagtc ctaaaaaatg tcctctcccg gaaaaacata cacatatact tgttcatggg 240
gacgatttca gtgtgaatag gcaagtttct gtgtcatgtg cagaagggta tacctttgag 300
ggagttaaca tatcagtagt tcagcttgat ggaacctggg agccaccatt ctccgatgaa 360
tccttgacgc cagtttcttg tgggaaacct gaaagtccag aacatggatt tgtggttggc 420
agtaaatata cctttgaaag cacaattatt tatcagtggt agccttgcta tgaactagag 480
gggaacaggg aacgtgtctg ccaggagaac agacagtgga gtggaggggg ggcaatatgc 540
aaagagacca ggtgtgaaac tccacttgaa tttctcaatg ggaaagctga cattgaaaac 600
aggacgactg gacccaacgt ggtatatctc tgcaacagag gctacagtct tgaaggggca 660
ctcagggacc actgcacaga aaatggaacc tggagccacc cagtccctct ctgcaaaacca 720
aatccatgcc ctgttccctt tgtgattccc gagaatgctc tgctgtctga aaaggagttt 780
tatgttgatc agaattgtgc catcaaatgt agggagggtt ttctgtctga gggccaccgc 840
atcattacct gcaaccccca cgagacgtgg acacagacaa gcgccaaatg tgaaaaaatc 900
tcattgtggt caccagctca cgtagaaaaa gcaattgtct gagcgctaca ttatcaatat 960
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gtttgtttag aaaaatggaac atggacatca cctcctattt gcagagctgt ctgtcgattt 1080
ccatgtcaga atgggggcat ctgccaaacg ccaaatgctt gttcctgtcc agaggctgtg 1140
gtggggcgcc tctgtgaaga accaatctgc attcttccct gtctgaaacg aggtcgctgt 1200
gtggccctct accagtgtga ctgcccgccct ggctggacgg ggtctcgctg tcatacagct 1260
gtttgcaggt ctccctgctt aaatggtgga aaatgtgtaa gaccaaaccc agtcactgt 1320
ctttcttctt ggacgggaca taactgttcc agggaaaagg ggaactgggt ttaaccactg 1380
cacgaccact cggctctccc aaaagcagga tcatctctcc tcggtagtgc ctgggcatac 1440
tggaacttat gcaaaagaaa tccaacatgg tgcgtgggtct tgtttagtaa acttgttact 1500

tggggttact ttttttatat tgcgatatat tttgttatc cttgtgacat actttcttac 1560
attgtttccat ttttaaatat gctgttatat tctatataaa aatatattata aatagatgct 1620
gcttaccact cacaataatt acatattctg ctgtctattg ggaaggttcc tggtaacacat 1680
ttttattcag ttacttaaaa tgatttttcc attaaagtat attttgctac taaataaaaa 1740
aaacgcg

```

1747

(2) INFORMATION ON SEQ ID NO. 114:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1526 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```

cgagccca ggccecgag tagcagcggg gaggcggga gccgcgggc cggagccgc 60
cggcgcaggc gtgggggctg cggggccggc ccatccgtgg gggcgacttg agcgttgagg 120
gcgcgcgggg aggcgagcca ccatgttcag ccagcagcag cagcagcagc tccagcaaca 180
gcagcagcag ctccagcagt tacagcagca gcagctccag cagcagcaat tgcagcagca 240
gcagttactg cagctccagc agctgctcca gcagctccca ccacaggccc gttgccatgg 300
tgtcagcggg ggtcccccgc agcagccaca gcagccgctt ctgaatctcc agggcaccaa 360
ctcagcctcc ctccctcaac gctccatgag gcagagagct ttgcttttac agcagttgca 420
aggactggac cagtttgcaa tgcccaccgc cactgatgac actgccggtc tcaccatgcc 480
cacagcaaca ctgggttaacc tccgaggcta tggcatggca tcccaggccc tcgcagcccc 540
cagcctcaca ccccccacaac tggccactcc aaatttgcaa cagttcttcc cccaggccac 600
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tgaggaaagg gcagagccccc ggatggacac accagaagac caagatttac cgccctgccc 840
agaggacatc gccaaaggaa aacgcactcc agcacctgag cctgagcctt gtgaggcgctc 900
cgagctgcga gcaagagagt tgaggagctc agaagagccc acagagaagg aacctccagg 960
gcagttacag gtgaaggccc agccgcaagg cggatgacag taccgaaaca gacacagaca 1020
ccagacctgc tgcctgagggc cctggaagcc caagtgtctc cagcattcca gccacgggtc 1080
ctgcaggtcc aggccccaggt gcagtcacag actcagccgc ggataccatc cacagacacc 1140
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cagccacagg tacagccaca gccacattca caggggccaa ggcaggtgca gctgcagcag 1320
gaggcagagc cgctgaagca ggtgcagcca caggtgcagc cccaggcaca ttccacagcc 1380
ccaggggagc gtgcagctgc agctgaggaa gcaggtccag acacagactt ttcacaggt 1440
gcacacacag ggcacagcca agcttccagg cacagggagc ttcttccggg cgcggtgtc 1500
agtttcaggc caccaggggc agggccc

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1526

(2) INFORMATION ON SEQ ID NO. 115:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1205 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

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cccgagaaaa accaatTTaa tgcttctgtt ctcagcattt cacagcatgc aggactcaaa 60
tggatacaac agaagaaaaa aaccocaaat ttttggaaaa ccctttgttc aatgattcat 120
attttgatat ctattgacaa tcccttagaa ctttaaattc caaaaacaaa aaagtactgt 180
ggatctccct cgagccgaat tcggctcgag ggcggtcacc tggagatgag aaaggcccg 240
gggggggacc atgtgcctgt gtccacagag cagccgagag gcggggagga cgctgctgcc 300
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tcccacagtg tggtagaaag tcttgaaata acacttttgc ctttcaaaaa aaaaaaaaaa1200
aaaaa 1205

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(2) INFORMATION ON SEQ ID NO. 116:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3968 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

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3968

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(2) INFORMATION ON SEQ ID NO. 117:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 798 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

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agattgtcca aacttagcag tatggtccat ctggtgtaga agtggaagtg tcatacaggal80
tagcaaacac tcttgggttc tttttgccc ggccttgccc gagccggcaa cagcaacaaa240
atgtggagga tgcaatgaaa gagatgcaaa agcctctggc ccgctatatt gatgacgaag300
atctggatag gatgctaaga gaacaggaaa gagaggggga cctatggccc aacttcatac360
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ctgtggtagt gggcataggc agcgagatat ccagtgttaa cagtgtgtct tgcttaaat660
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agacctgatg tttggattga ggtacctgtt cttcttgggg tgttgacagc agcgggtgtt780
ggtgggtttt cagaggaa                                798

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(2) INFORMATION ON SEQ ID NO. 118:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1068 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

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ccctctcttg tgactcagtc tctgagcgtt ttaatacagat ggtgtccccc cgggatcaaaa 60
cttcagcgctc acagctgagg actggctcttg tggctccctga tgggagagca tgaacagggtg 120
gtatgtgaag cccttgggaa ccagctcttc caaagtcaaa gccaaagacca ttgtgatgat 180
tcccgaactcc cagaagctcc tgcgatgtga acttgagtca ctcaagagcc agttacaggc 240
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(2) INFORMATION ON SEQ ID NO. 119:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 4584 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```

ctcgagccgc tcgagccgcg gaagtaattc aagatcaaga gtaattacca acttaattgtt 60
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agctgaccca ggtgctacac agaagtgatc tcagtgaatc taggaagaca gcagcagaca 180
ggattccagg aaccagtggt tcgatgaagct agggcttgagg gcaagagggc aagcagcagt 240
tggttggtgaa gataggaaaa gagtccagga gccagtcgca tttggtgaag gaagctagga 300
agaaggaaag agcgctaaag atttggtggt gaaaagagga attgggagtg gtaggatgaa 360
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gaccttatat agggaaaaaaga tga

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(2) INFORMATION ON SEQ ID NO. 120:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 982 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```
gtggaggggga cctctgtggtt agcagcagct atcgacagct cggatgttca gagcagcaga 60
agcggcgctgc gtctgattgtt gtgttgcccg ccaccatgag ctacacaggc tttgtccagg120
gactctgaac cactttgcag tcgacatact cggataccag cgctcagccc acctgtgatt180
atggatattgg aacttgggaac tctgggacaa atagaggcta cgagggctat ggctatggct240
atggctattgg ccaggataac accaccaact atgggtatgg tatggccact tcacactctt300
gggaaatgcc tagctctgac acaaatgcaa acactagtgc ctctgggtagc gccagtccc360
attccgtttt atccagaatt aaccagcgct tagatatggt gccgcatttg gagacagaca420
tgatgcaagg aggcgtgtac ggctcaggtg gagaaggta tgactcttat gaggctcgc480
actcgagggc cgtctctgagt gagcgcgacc tgtaccggtc aggcctatgac tacagcgagc540
ttgacctga gatggaatg gcctatgagg gccaatagc tgacctaccg gaccagtctcc600
gcctcgctgg caacgacacc ttctgtccca gggcacaggc ctgggcccgg gatgcccgga660
gcggccggcc aatggccgca ggctatgggc gcattgtgga agaccccatg ggggcccggg720
gccagtgcct gtctgtgtgcc tctcggttgg cctctccctct tctccagaa catcatcccc780
gagtagcgca tgttccaggg gcctcgagg ttggggcgcc tcccgggcg gcttccgctt840
ttggttttcg ggttttgcaa tggcatgaag cagatgaggg cggaactggga agacggggac900
cacagccgat ttgcgaacca agaagaagaa gagaagcag ggcggcattc tgattgagcc960
agttagcaaa gcagccggaa tt                                     982
```

(2) INFORMATION ON SEQ ID NO. 121:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 742 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual
 ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

```

ctcaacttcg  cagcactcgc  tgcctcaagc  cgacgcagcg  gcctactctc  gcactgcaga  60
cggggaaact  gagggccgag  gcggccgggg  tggggcagac  ctcccggcga  gcccgagccc  120
ccgcccccg  ctgccccgc  cctggcccg  aagaagcacc  cggggcgcga  ggcgaagcgc  180
cacagcgcg  ggccagcgt  ggtccagcag  cgcgatggca  gctcagcgcc  tgggcaagcg  240
cgtgctgagc  aagctgcagt  ctccatcgcg  ggcccgcgcg  ccagggggca  gtcccggggg  300
gctgcagaag  cggcacgcgc  gcgtcacogt  caagtatgac  cggcggggag  tgcagcgggc  360
gctggagcgt  gagaagtgg  tcgacgggg  cctggaggag  ctgtaccgcg  gcatggaggc  420
agacatgccc  gatgagatca  acattgatga  attgttggag  ttagagagtg  aagaggagag  480
aagcgggaaa  atccagggac  tcctgaagtc  atgtgggaaa  cctgtcgcag  acttcaccca  540
ggagctgctg  gcaaaccttc  aaggcctcca  caggcagccc  ggcctccgcc  agccaagccc  600
ctccccgac  ggcagcctca  gccccctcca  ggacggggcc  cggactgctc  acccctgacc  660
ctcttgact  ctccctgccc  cccggacgcc  gccagcttg  cttgtgtata  agttgtattt  720
aatgggtctg  taacaataaa  aa

```

742

(2) INFORMATION ON SEQ ID NO. 122:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2330 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|--------------|------|
| gtttggacaa | gttgttttaa | taggaatat | acctgcgtgc | ttcataggtt | tcctcaacca | 60 |
| cttttcccca | gctttcttaa | aatgggatct | acattggtgc | ttcacaccca | aatagcagac | 120 |
| taactgtttt | tctgttagc | accgtctggg | tcattgtctt | gaactctgcc | ttacagcagc | 180 |
| aagaaaaatt | tcctgcacaa | gaacctcaat | ctttagtccc | attgagctcc | ccctctggat | 240 |
| tttggactta | ccagaagttag | gaggttctga | taccattcaa | gatggctctt | ccttcaaaagc | 300 |
| aggctctgaag | aggagactac | caaagcagtg | tttcaaaacc | cagagctcac | acaacctat | 360 |
| tgcatagaac | agcacttggc | tttcacaagc | ctcctacagg | acctggtgta | attggagtag | 420 |
| aagggcagag | accctggagc | tggaggtggc | tggtgtgctg | gatgggaaga | aggcagaagg | 480 |
| ccagggggct | ttggacatag | agcaggggtg | aagctgcaag | tactgggaag | gaagagagtt | 540 |
| tcacagaaac | aaagctttgt | cacacagaaa | tgagttctgt | ctcactgggt | acctcatccc | 600 |
| tcaggctcca | gctgagcaga | gattttaatc | agcttccctt | atgggtattg | acactgctca | 660 |
| ggaagcagta | gacctgtgca | gggacagcta | ttgatctttt | gtgttctgat | tagattggaa | 720 |
| aatagatcaa | cttcattgta | gtccaggaac | tggttggtcac | agctactagg | aatgaggtga | 780 |
| tttctgaggg | ctgagaaaaa | acacagaatc | ttggccagca | gccagcagct | cccaggtgaa | 840 |
| agatgcattc | actttctcct | tgagagttgg | ggttgagggc | aaacatagaa | ccacaggttg | 900 |
| gctttacaac | cagtgctccc | gaagccctcc | ttcgggagaa | ctgtaagtaa | gaggtgggtg | 960 |
| tgtctaaaga | caataccatt | aatgaatggt | ctggccttac | ctaaaaaggt | ttagcaattt | 1020 |
| ggggataact | cttggatcta | gcttatgtgc | gttcacatgc | acatttgccta | gcccagagctt | 1080 |
| tttaaaatga | gggtctggcat | atacttgatt | acaaatgaaa | actcagaaaac | caattttattt | 1140 |
| tattaaatca | tatcttttgt | ttttccccct | cccttctaata | cccccaaaag | acctatttga | 1200 |
| gctgtttcccc | aatctcatctg | cttatttttg | accatgaatc | tgccagagtg | atatattctgt | 1260 |
| ttatttctcc | tcctaaatctt | tcctgtatgt | ttccaataaa | gattttaactg | gggtggccccct | 1320 |
| taaggtgaca | tcaggatgct | cttatgtcct | tcacagaataa | gcatacacct | catcctctctc | 1380 |
| ccctttccat | ccctctgcat | tcctaatctc | ttgtctttct | cactttggagc | cgaggggtgct | 1440 |
| tttagagaggt | gggtttcccat | gaatcagcca | agatttctctg | agaagtgggt | tacacatttt | 1500 |
| ccagtttcaa | agctctctcg | ctatgctaatt | gtccccctcag | agatgaggtt | tgacttttag | 1560 |
| gcccgtatga | ctcctccata | gcttggccaa | ggagaccatg | agttagccatg | tctggtttac | 1620 |
| tcctttatcct | gagactgttt | gttttatagct | taaaaacagaa | gtgtgtcttc | ccagcacaaa | 1680 |
| cctaatacaat | cagtgatca | gtgcatctgg | tggcaacagc | tcagcccatt | caaaagacaa | 1740 |
| ggattcagga | aaggcacact | gatgggtggg | agcctcttaa | gagcctctaa | tgttctccca | 1800 |
| aaacacagag | tgagagtggg | agtgccagt | gtcggggccc | actattcctg | aataaaggga | 1860 |
| atgcaagggt | cagaagttagc | ttgactctcg | cctaataatc | tgtgcctttg | cctgtccttt | 1920 |
| ctcccactct | actgaaaacc | ggaacagatt | cccgcttgcc | ttctgatgaa | gagaggttag | 1980 |
| gtaaaagagag | tttggaggaa | aaaagacacc | aggaggcagg | ctgtggggta | ggagaggggt | 2040 |
| ctgagagggg | gcagcaatcc | agaataacct | ctttcttagc | cagcatccct | tgaaactttt | 2100 |
| aaaggtctgt | gctaccactg | gctggcacac | cagggcaatg | atttccccgc | agaagggaag | 2160 |
| aaagaaatggt | ttcacccctg | catccttctt | gggagaagct | accagcctgt | tgcttcagtt | 2220 |
| tgagttgggt | tcacattcag | gattttgggg | ttttatgggt | tttctctctc | ccctgtgttt | 2280 |
| tgccccgaac | gttgatcaac | agggttgaaa | aagggccacc | tgagggtttc | | 2330 |

(2) INFORMATION ON SEQ ID NO. 123:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1860 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

gaggcagttt gagatcacca gcatttcogt ggatgtctgg cacatcctgg aattcgacta 60
tagcaggctc cccaaacaaa gcctcgggca gttccatgag ggggatgcct atgtgggtcaa 120
gtggaagtcc atggttgagca cggcagtggt aagtcgccag aagggaagagc actcgggtgag 180
ggcagccggc aaagagaagt gcgtctactt cttctggcaa ggccggcact ccaccctgag 240
tgagaagggc acgtcggcgc tgatgacggt ggagctggac gaggaaaggg gggcccaggt 300
ccaggtttcc cagggaaagg agccccccctg tttcctgcag tgtttccagg ggggagtgtg 360
ggtgcactcg gggaggcggg aagaggaaga agaaaatgtg caaagtgagt ggcggctgta 420
ctgcgtcggt ggagaggtgc ccgtggaagg gaatttctgt gaagtggcct gtcactgtag 480
cagcctgagg tccagaactt ccattggtgt gcttaacgtc aacaaggccc tcacttacct 540
gtggcacgga tgcaagccc aggccccacac gaaggaggctc ggaaggaccg ctgcgaacaa 600
gatcaaggaa caatgtcccc tggaagcagg actgcatagt agcagcaaaag tcaacaataca 660
cgagtgtgat gaaggctcgg agccactcgg attctgggat gccttaggaa ggagagacag 720
gaagagcctac gattgcattgc ttcaagatcc tggaagtgtt aacttcggcg cccgctgtt 780
cactctcaag agctcctctg gggattttgc agccacagag tttgtgtacc ctgcccgagc 840
ccctctctgt gtcagttcca tgcccttctc gcaggaaagt ctgtacacgg cgccccagcc 900
agcacttttc cttgttgaca atcaccacga ggtgtacctc tggcaaggct ggtggcccat 960
cgagaacaaag atcactgggt ccgcccgcac ccgctggggc tccgaccgga agagtgcgat 1020
ggagactgtg tccagctact gcaaaaggaaa aaatctcaag aaaccagccc ccaagtctta 1080

ccttatccac gctgggtctg agccccctgac attcaccaat atgtttccca gctgggagcall40
cagagaggac atcgtctgaga tcacagagat ggacacggaa gtttccaatc agatcacct1200
cgtggaagac gctcttagcca agctcctgtaa aaccatttac tctatctcac cgacgaagac1320
caggccactc ccggagggggt gcgtcctctg aagcttgaga ccttgccccc ctgggaagcag1380
gtgcaacctga agaaagcaaaa agccctgttc tgagtgggga atatttttgg actggtgttt1500
gtcacgtcca acaacaccac tgcaaccagg aaatggatat attgttaagg atactgctgt1560
ttcacaaagt atttttcaat cacagttttc agaacctgac ttggaaaact ctttccacca1620
tcccgagatt ggtgtattttg taaatgttca agggaactgt gcaacttaagc cgcagctgct1680
ttcaggaggt tatcagaagt aataaaaagta tctgttatgt tttttttttt tttagaacag1740
atagatagca ctgccttctt gttccagcta ggcaatgcct tttttttttt ataagtcaaa1800
ttctctttat aaagtgttat ttgatagtt tgtggattct aaatacccat gttgtttttt1860
tatggattta acaagcaaat atgtattcat tcaatttcca gatttggggg gttgtttttt

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(2) INFORMATION ON SEQ ID NO. 124:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 807 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```

cctttctctca tctctattaa attgtaaaca ggactactgc atgtactctc tttgaggtga 60
atttgggaatg gaaggccagg gactatactc tttttaaaaat agacatttgt ggggctcaca120
caatatatga aatagtagcc tctaaaaaagg agaaaaaaa aatcaggcgg tcacacttag180
agcaacattg tcttattaaa gcatagttta tttcactaga aaaaatttaa tatcaaggac240
tattacatac ttcattacta ggaagtctct tttaaaaatga cacttaaaac aatcactgaa300
aacttgatcc acatcacacc ctgtttatct tctttaaaca tcttgggaagc ctaagcttct360
gagaatcatg tggcaagtgt gatgggcagt aaaataccag agaagatgtt tagtagcaat420
taaaggctgt ttgcaccttt aaggaccagc tgggctgtag tgattccttg ggccagagt480
gcattatggt tttacaaaaa atgacatat gtcacatggt tgcattgttg tttgctgttt540
gaatttttga acagccaggt gaccaatcat agaaagtatt accttctttt atatggtttt600
tgggttcactg gcttaagagg tttctcagaa tatctatggc cacagcagca taccaggttt660
ccatcctaag agggaaatgga aattaatttt gtaacctact gattaacaga atctgggggt720
cacattggaa aaaaattctt ttatcgtctt ttaaggata tgtttaataa ttattttatg780
tgtcggcata ttgcggcagc tctgaga                                     807

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(2) INFORMATION ON SEQ ID NO. 125:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1932 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```

ccgggggtttt gggctggaac tgcagcgctt agagagctcg gtggaagctg ctaaaggcgg 60
aggcgggggct ctggcgagtt ctctctccac ctccccccac ccttctctgc caacgcgtgt 120
ttcagccctt agctggattc cagccattgc tgcagctgct ccacagccct tttcaggacc 180
caacaacccg cagcgcgtgt tcccaggatg gtgatccgtg tatatttgc atcttctctt 240
ggctctcacg cgattaagaa gaaacaacaa gatgtgcttg gtttccatga agccaacaaa 300
ataggatttg aagaaaaaga tattgcagcg aatgaagaga atcggaagtg gatgagagaa 360
aatgtacctg aaaatagtgc accagccaca gggtaccccc tgcccacctc gattttcaat 420
gaaagccagt atcgcgggga ctatgatgcc ttctttgaag ccagagaaaa taatgcagt 480
tatgcttctt taggcttgac agccccacct gggtcaaaag aagcagaagt gcaagcaaa 540
cagcaagcat gaaccttaag cactgtgctt taagcatcct gaaaaatgag tctccattgc 600
ttttataaaa tagcagaatt agctttgctt caaaaagaaat aggcctaatg ttgaaaaaat 660
agattagtgt ggttttcaca tgcaaacatt caaaatgaat acaaaattaa aatttgaa 720
ttatggtgat tatggtgagg agaatggggt attaacataa aattatatta ataagtaga 780
atcgtagaaa tagtgttgtt acctgcgaag ccactcgtga tacaccaatg attttacaaa 840
gaaaacaccc ttccctcctt ctgccattac tatggcaact taagtgtatc tgcagctcta 900
cattaaaaag gagaagagaa aataacctgt ctctcattcc taagtgtcct cattatatt 960
catgaacaag aatatgtacc tttttgatgc tatattactg cgattaaaaa gttcttgcag 1020
gtaattgttta tgatatgtta aacgttgtaa tttctatcog taattataac attcccatatt 1080
ttttgtagat gaaccttcta catattgaac cacagatttt ctgagctctt aaatgtagcc 1140
tttcattgca catttcagtg atcagaatag atatcctttt acacgcacaa aagcaataga 1200
ttcattcagt ggacaagttc cttgtttaac tacacagctg tgatggaaat atatatccaa 1260
gttccctggc tcaagtgaat atgcatagtc atatcatgaa agtgggatgc caagtaagct 1320
taaaatggca ttctctagca aagagattag actttttaa aactgtataa aaacaggtg 1380
ggcatcattt cccaagattg gtttcccttg agtttttgct aaaaacaaatc ttagtagatt 1440
tgcccgttta aaacaactca caatcgtaaa tgctactatt cctaagatat cttacctttt 1500
tatttcagtt tagccatgta ttgtatgagt gtattagtct aagcagtgag aatcttttct 1560
atgcctctat tccagcaaaa agtagaagta tcaaatataaa agggccaact ttaaaatatt 1620
aagccctgaag acttctaaaa agacaagaaa catggccctaa ataaaccaac tagatttaca 1680
tagtaagttt cacactacct tattaccaaa agcaaaacac tcttacttta aactacatta 1740
tcatgtatat ctattgtatg ctggtcttta ctttttgcca aaatcaacat ataatgaag 1800
gatgcctttg tttcatgaga ttcaaaactg atgctatgct ttaaaataaa ctaagtactt 1860
ttagaaacat aaaaaaaaaa aaaaaaagcg gacccccoga gtatgtgggc cgcgccgggg 1920
gatttttccg gg

```

(2) INFORMATION ON SEQ ID NO. 126:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3024 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```

atatatgttta agacattccc ttgctaatta ttttctcttc tgttgttcta tttttttggt 60
ccagtttgct gtttttaaaag ttttgagtc cagctgggtcc tgtacattta actgaaaaaa 120
aagtaacttta aaataatata aaaatagcac tcattgtatgt cctacagtta taggtgaaat 180
ttgataattgt ttgtctttaca tagcatacct atagacagct taagttaaagt gactgttaaag 240
aggggttatgc ttatttgatga actctgttag ttgtttacca gctctgttag tatagttaa 300
ttgatctcag tagcttcaag tatttataaa atggttgaag tccaaataca tgtgataatt 360
acaaacacact ttgaattaat ggggggtggg aggctagttg aaatgcattt tatttaccoc 420
aggagtatgt taaaatgata gttataaatg ttgggaagttt aaagcaagat actcagttta 480
gttcttttaca aatcataaga agaacaaaat tagatgttga cattgtctatt tttaggtgtg 540
tggtttccat atgcttcttg ctttccctgt cacaggtggt gccagcaata ttggtgtgat 600
tgagggttat ttggcaccac tcgcacacag gcgcacaatg gtgttagctg gccagaaaga 660
gtggcatcttc tggctaccgg gctgggggcg acctttacca taggtagaag taacctgtga 720
ttcggctgca aggtgtactg tacgtacaca ggtgctggct gatgtccact ttctgctttt 780
ctttctttct tttttctttt ttaaaagtaa tttcccccac agtaaaatcac actgactcct 840
gagtaaatgt attttccagt ttatggaaat tgggaagtctg acaagtgaaa ccaatttaat 900
gtaaagtatt tggccttcaa atggtttctc tgtgctattt ttgggaattc ttccagattc 960
cagagatatt ttacgtcttt gattcaattt aaaaatttga cttattttct tttagaaatal 1020
atgtattgtg tctgtgcaga aaaaaaaaaa ccaaaaaggga ttgctttact ccaagaggag 1080
agattgtctt aggataaaac tccaaagcca catttaatat aacagactga agtaaacatt 1140
agaaatctgt tttagactat tctgcacagt taactactga tctttagaat ctaaaaattg 1200
atatgaacct attcttaaat aattgaaccg ttttatattc aaatgactta tgatcggtgt 1260
tagtttggga aaaaataagat ggttaaattt tgatttaatt aaagttaatt gtattttttt 1320
cataaaatag cattttcaat ttgtaattgt gtttaacatc cttgtgtgtt gccaaagaaa 1380
ttctatttgg ctgtgaatat tctatttgcg tgcagtatct gtctctcttc ctaggctcaa 1440
gttggtgacc caagcctatt gtaaaccaat gattatctca aaggagatg ccaatggagt 1500
aacaaattgt taaccttcag ttttctgtct gtatatcttt ttaaaaaatc ggtagtttct 1560
ggaaaaaaaa gagaaggggg ttgtgtgtac ttaaccttat ttatttccgt atattttagt 1620
taattagttt ttggaataaa tggatttcag tatagctttg tggttaaatt gcattgacct 1680
tattttatgt ttaggcttat tttaaatata acattttaaca gaacactttg aactagaatt 1740
tgcatgtctg ccttaataaa cttaaagact gattttaatc tgactatgac actgagcata 1800
ttctttaaat tactcataat ttaataatgt taataatac taatttaaat tttagcagttt 1860
tagtataaga ttgtgcattt tgtctctgtg atgtctgaat gaagctataa cacttgacct 1920
tttatgcag gttttccctt ggaatatgga taaatacacc atgatacga aactgaagg 1980
acatcaccat gatgtggtag cttgtgactt ttctcctgat ggagcattc ttggtcactg 2040
atcttatgat actcagatg atatctggga tccacataat ggagacattc tgatggaatt 2100

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tgggcacctg tttccccac ctactccaat atttgctgga ggagcaaatg accgggtgggt2160
acgatctgta ccttcttagcc atgatggact gcatgttgca agccttgctg atgataaaat2220
ggtagaggtc tggagaattg atgaggatta tccagtgcaa ggtgcacott tgagcaaatg2280
ctctttgctg gccttctcta ctgtagggcag tgttttagct gctggggacac atgacggaag2340
tgtgtatttt tggggcaactc cacggcaagt ccttagcctg caacatttat gtgcgcatgc2400
aatccgaaga gtgatgccca cccaagaagt tcaggagctg ccgatttcctt ccaagctttt2460
ggagtttctc tcgtatcgta tttagaagat tctgccttcc ctagttagtag ggactgcag2520
aatacactta acacaaacct caagctttac tgacttcaat tatctgtttt taaagacgta2580
gaagatttat ttaatttgat atgttctgtg actgcatttt gatcagttga gcttttaaa2640
tattatttat agacaataga agtatttctg aacatatcaa atataaaattt ttttaaaagt2700
ctaaactgga aaacatacat acctgtacat atttagatat aagctgctat atgttgaagt2760
gaccttttgc cttttctgat ttttagttct gacatgtata tattgttcca gttagagccac2820
aatatgtatc tttgctgtaa agtgcaagga aattttaaat tctgggacac tgagtttagat2880
ggtaaaact gacttacgaa agttgaattg ggtgaggcgg gcaaatcacc tgaggtcagc2940
agtttgagac tagcctggca aacatgatga aacctgtct ctactaaaaa taaaaaa3000
aaaaaaaaa aactcgaaac tact 3024

```

(2) INFORMATION ON SEQ ID NO. 127:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 505 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

ctgcacgggc gcagatgtag gcaccggctc gactgcctgc cctctgtccc cggggctggg 60
tctctgtctc tccggttcct gggctcctaa tctctgttcc agcttcttcc aggtctgcgc120
gtctgttggt cccagcgctc tgcgaagctg aaaaaggagga gcaacctgtc cagaatcccc180
gcaggacagc aaaaaggagg gaaatctcga catggaaaaa ctctacagtg aaatgaagg240
aatgcttcca aaccaggaa agatggaaaa tgaagaacag ccacaagcag agagaaaagcc300
agaagtaact tgtactctgg aagacaagaa gttgaaaaac gagggaaga cagaaaaaa360
gggcaaaaaa ggagatgagg aaatgttaaa ggataaagga aagccagaga gtgaggaga420
ggcaaaaaga ggaagtcag agagggagg agagtcagag atggaggagg tcgagagaga480
gggaacccga ggtaggggaa gcgga 505

```

(2) INFORMATION ON SEQ ID NO. 128:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

PPLRLRLEFFY LRFISTSTA EIRKWRFGQ IILYEMDPHT TSFLIQARYN IIPGFSKSSQ 60
 HGYLECYSVLA FIAASSERRA FFSKFKLVKV SCLWAAFLPS ITMKMHPTTV RAIIR 115

(2) INFORMATION ON SEQ ID NO. 129:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

VRDGAPGLSC GFVQNPFILF KSELLVSLAD EETSLSHNLK QLPAARRRPL RLPMATCYSA60
 DQRRTPGTV ALVSSMSPSV GV 82

(2) INFORMATION ON SEQ ID NO. 131:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

GIITLSLLMI IHPQMEEFIR QPLQFRLKTG AHRTQGTIKE DQEPFFLSK NWP

53

(2) INFORMATION ON SEQ ID NO. 132:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

LFILRWRSLS VSHFSFVLKQ EPTGPKELLR RTRNLGFFFQ KIGSPINEG KN

52

(2) INFORMATION ON SEQ ID NO. 133:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

KKKPRFLVLL NSSLGPGVSC FKTCLKWLTD KLLHLRMNNH Q

41

(2) INFORMATION ON SEQ ID NO. 134:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

ADPAFSTDLF QGCTDMAAAF RKAAKSRQRE HRERSSDYRK KQEYLKALRK KALEKNPDEF 60
 YYKMTRVKLQ GGVHIKETK EEVTPEQLKL MRTSGRQIYR KGRGCRS 107

(2) INFORMATION ON SEQ ID NO. 135:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

RIRRSPLIFS KAVQTWRLRF GRRLSPGSGN TESEAVTTVK NKNTSKLEGR RLLKKIQMNS60
 TTK 63

(2) INFORMATION ON SEQ ID NO. 136:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

LFWGYFFLSL LNNMYSTLEF NPSHFVVEFI WIFFKSLLPK SFEVFLFFTV VTASLSVFPL60
PGLSRLPKSR RHVCTALEXI SGERRIR 87

(2) INFORMATION ON SEQ ID NO. 137:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 95 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

EANNYMSCQG GSRFHSFSIL PQYPGINAAT GGQSLFVLLP TPLFLCLFNS VKLFCLGPCK60
EPKENLSGQV HEWNAENILK ARFLEYSQLA FFPLI 95

(2) INFORMATION ON SEQ ID NO. 138:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 77 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

NSSASSPQFW PNSRLAVFTW YPGVGLLTLLI SMMFSKMKLD KVDHQLHRVF CKSIVSKWPR60
DLRKIQIFCL PWSCFKS 77

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 133 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

DLKQDQGGKQK ICIFLKS LGH LLTILLQKTR CSWNSTLSSF ILENITIEIKV SNPTPGYQVK 60
 TASLLLGQNC GLLAELFYGL QSKWSYLTHK MTKVLNLVRG KVLNIQFWIQ EIIIVNFPFK120
 SMERMLVENI LK1 133

(2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 783 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

FLLPQSAFHL YEPPLDYMT WRMGPRTML LAMWLVCSE PHPHATIRGS HGGRKVPVLS 60
 POSSRPARFL RHTGRSRGIE RSTLEEPNLQ PLQRRRSVPV LRLARPTEPP ARSDINGAAV120
 RPEQRPAARG SPREMIRDEG SSARSMLRF PSGSSSPNLL ASFAGKNRVW VISAPHASEG180
 YYRLMMLLKK DDVYCELAER HIQIVLFHQ AGEEGGKVRR ITSEGQILEQ PLDPSLIPKL240
 MSFLKKLEKKG FGMVLLKKT L QVEERYVPV RLEAMYVID QGPIRRRIEKI RQKGEVQCKK300
 ASGVEGQVVA EGNDDGGGAG RPSLGSEKKK EDPRRAQVPP TRESRVKVL R KLAATAPALP360
 QPPTSPRATT LPPAPATTVT RSTRAVTV A ARPMTTTFP TTQRPWTSPS SHRPPTTTEV420
 ITARRPSVSE NLYPPSRKQD HRERPQTTR PSKATSLSEF TNAPPTTISE PSTRAAGPGR480
 FRDNRMDRE HGHRDPNVVP GPPKPAKEKP PKKKAQDKIL SNEYEEKYDL SRPTASQLED540
 ELQVGNVPLK KAKESKKHEK LEKPEKEKKK KMKENADKL LKSEKQMKKS EKKSQKEKEK600
 SKKKKGKTE QDGYQKPTNK HFTQSPKKS ADLLGSFEGK RRLLLITAPK AENNMYVQQR660
 DEYLESFCMK ATRKISVITI FGPVNNSTMK IDHFQDNEK PMRVVDDEDL VDQRLISELR720
 KEYGMTYNDP FMVLTDVDLR VKQYVEVPIT MKSVFDLIDT FQSRIKDMEN QKRGVFEGG780
 KTP 783

(2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

KMVVGVMVFL RWERMENLF QGNGFAAEVR MCSCIDLQTP RRWVHTACLG VPRDSRPPTY60
 LSEARAAGHG PSAKPVCDAL GALVQEA 87

(2) INFORMATION ON SEQ ID NO. 145:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

SFSSGLVRNT LFITTFKFLY FFSSMLVLMT EGDVSVRAGE RGVRRPSHRW SWPPPALSLL60
 PDHRFPICPS ENLSQGELKF TGQGTSTFIYF IMLANRT 97

(2) INFORMATION ON SEQ ID NO. 146:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

ASCTKAPRAS HTGLAEGPWP AARASDKYVG GLESLGTPKH AVCTHLLGVC RSIQEHILTS60
AANPFPWKRF SHILSHLKKT HTPTTIF 87

(2) INFORMATION ON SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 119 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

NSKDKCFSLA FITTPETERW RCCASEPRL ALKHQGHRTQ AWQRGHGQRH ELQTSMLEVS 60
NPLAPPSMQC APTFWVSADR YRNTSLPLQR THFPGKDFHT SSPTSKKPTH PQPFFKAPR 119

(2) INFORMATION ON SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 87 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

STKGIAHRLG RGAMASGTSF RQVCWRSRIP WHPQACSVHP PSGCLQIDTG THPYLCSEPI60
SLEKIFTHPL PPQKNPHTN HFLKPHG 87

(2) INFORMATION ON SEQ ID NO. 149:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

DPPSHSQLGR CCHRMVFESV GARAHFWLSQ QLGWHLPLSA RNSNIMNARD SVLSKVFHFK60
GAGHGCSRL 69

(2) INFORMATION ON SEQ ID NO. 150:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

SAHLGLPKCW DYRREHPCPA PFGWKTLLST LSLAFIMLLF LALGSKCHPS CCDNQKCALA60
PTLSNTIR 68

(2) INFORMATION ON SEQ ID NO. 151:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

HHTQPIFVFL VATGFHHVQG AGLEPLTSGD PPTLASQSAG ITGVSTRALP LLDGRLY 57

(2) INFORMATION ON SEQ ID NO. 152:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 57 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

SAGIPKLAPK IPLPFSOLLK CYLISGAFFD HTLKTSTPTH GPCPPSRLHF LAYTYQM 57

(2) INFORMATION ON SEQ ID NO. 153:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 32 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

LKTLTVASI RVSTFYSSDP TSFNLLLLLY GG

(2) INFORMATION ON SEQ ID NO. 154:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

TKRAVMKSMH LCAIRAFLLVP HSELIDSDYI HF

32

(2) INFORMATION ON SEQ ID NO. 155:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

GRVRAVKGRH SDRSHSQQCQF QSVNTDEVPT T

31

(2) INFORMATION ON SEQ ID NO. 156:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

VQNVMSACNF IFIKAKLIYM EYCSIYYAPI YILSPVVRYF ISLLLNIFYT YL

52

(2) INFORMATION ON SEQ ID NO. 157:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 59 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

TGTECFFICC IENSHTQFSI LQCSHHGWT LGRNSPQPFL VSFSQFFSVS RWAPVINLP 59

(2) INFORMATION ON SEQ ID NO. 158:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 38 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

LSLCPWPNGN FFQWCLLEEV FSSGQFKEIK LGNGEGGR

38

(2) INFORMATION ON SEQ ID NO. 159:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

GSILMMQEI SSWSQKFPRG AVFLRNGVYL NNS

33

(2) INFORMATION ON SEQ ID NO. 160:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

KKLPQGQGHK LNYLNLKLF LKIQHLLGTF DSRKRFPASY PKCF

44

(2) INFORMATION ON SEQ ID NO. 161:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 225 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

AAGGLGLGVG PRGMWRAGSM SAEGLVGCAL RAVNERVQQA VARRPRDLPA IQPRLVAVSK 60
TKPADMVIEA YGHGQRTFGE NYVQELLEKA SNPKILSLCP EIKWHFIGHL QKQNVNKLMA120
VPNLFMLETV DSVKLADKVN SSWQRKGSPE RLKVMVQINT SGEESKHGLP PSETIAIVEH180
INAKCPNLEF VGLMTIGSFG HDLSQGPNDP FQLLLSLPEE TVVKS 225

(2) INFORMATION ON SEQ ID NO. 162:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 99 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

CRGPGARRRS PGDVESWQHV GRAGSRVRIA GGERARAAGC GAAAAGSPSH PAPASGGQQN60
QTCRHGDRGL WTAAAHFWRE LASGTARKSI KSQNSVFVS 99

(2) INFORMATION ON SEQ ID NO. 163:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 120 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

LRSCPGLPMV ISPTNSRLGH LAFMCSTMAM VSEGGRPCLL SSPLVLIWTI TFNLSGEFFL 60
CQELFTLSAN FTSTVSSMK RLGTAINLLT FCFRWPMMC HLISGHKDRI LGFDFSSSS120

(2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

TSTGPFSSPLV ASAATELAAF AAFSSACMR PEGSASLFWN RLPLLMFGDL QGCEAREGIA60
 MRILQASFSG LSSKG 75

(2) INFORMATION ON SEQ ID NO. 165:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

NTHGDALTCL TPLQVPKHEE GKAIPKQRGR TFRHTCRAK GSGKSCQFSC SRGYQGAGGT60
 SAGLALYLHT RTAASRGTSF SPVGSVAPQQ 90

(2) INFORMATION ON SEQ ID NO. 166:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

SHPFEDSPEK EACKIRMAMP SRASHPCRSF NMRRGRRFQN REAEPGRIH AELKAAAKAA60
SSVAAEATRG LEGPVLV

77

(2) INFORMATION ON SEQ ID NO. 167:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 347 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

TAFPLFVVVA AVLWGAAPTR GLIRATSDHN ASMDFADLPA LFGATLSQEG LQGFLVEAHP 60
DNACSPIAPP PPAPVNGSVF IALLRRFDCN FDLKVLNAQK AGYGAAVVHN VNSNELLNMV120

WNSEEIIQQI WIPSVFIGER SSEYLRLAEV YEKGARVLLV PONTFPLGYY LIPFTGIVGL180
LVLAMGAVMI ARCIQHRKRL QRNALTKEQL KQIPTHDYQK GDQYDVCAIC LDEYEDGDKL240
RVLPCHAYH SRCVDPWLQ TRKTCPICKQ PVHRGPGDED QEEETQGQEE GDEGEPRDHP300
ASERTPLLGS SPTLPTSEFS LAPAPLVFFG PSTDPLSPF SSPVLV 347

(2) INFORMATION ON SEQ ID NO. 168:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 588 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

QVTNMSDKSE LKAELEKQKQ RLAQIREKK RKEEERKKKE TDQKKEAVAP VQEESELEKK 60
 RREAEEALLQS MGLTPESPIV PPPMSSESSKS VSTPSEAGSQ DSGDGAVGSR RGPiKLGMAK120
 ITQVDFPPRE IVTYTKETQT PVMAQPKED EEDDDVVAPK PPIEPSEET LKKEENDSK180
 APPHELTEEE KQQILASEEF LSFFDHSTRI VERALSEQIN IFFDYSGRDL EDKEGEIQAG240
 AKLSLNRQFF DERWSKHRVV SCLDWSSQYP ELLVASYNIN EDAPHEPDGV ALVWNMKEYKK300
 TTPEYVFHCQ SAVMSATFAK FHPNLVVGTT YSGQIVLWDN RSNKRTPVQR TPLSAAATH360
 PVYCVNVVGT QNAHNLISS TDGKICSWSL DMLSHPDQSM ELVHKQSKAV AVTSMSEFPV420
 DVNNFVVGSE EGSVYTACRH GSKAGISEMF EGHQGPITGI HCHAAVGAVD FSHLFVTSSF480
 DWTVKLWTTK NNKPLYSEED NADYVYDVMM SPTHPALFAC VDGMRGLDLW NLNNDTEVPT540
 ASISVEGNFA LNRVRWTHSG RGGGCGGILK DKFCYFAMLG GAVCWSPQ 588

(2) INFORMATION ON SEQ ID NO. 169:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 41 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

FHVEQLSHSF LSWRKDTIQR GSKDFVKRGI HNLLWSKCPH L

41

(2) INFORMATION ON SEQ ID NO. 170:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 55 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

CPRDVGTCISI VNYGCHVLQN PYCPFELCPs SKIRSYDSIV QHGIMKSLs SSIFP

55

(2) INFORMATION ON SEQ ID NO. 171:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

KAFLVLSFFK WALFLVIHMT LFGCGCLLNF LEWTSFSKPK PARDRKGNGN

50

(2) INFORMATION ON SEQ ID NO. 172:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

CTFNIESFIY LIVYRTFPHY THLLHNILTS IFKFFCTSSF SFNLVKPVIH TNVYCELG60

(2) INFORMATION ON SEQ ID NO. 173:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

EESFVFLIHS FVNRYKGTNV LTYTKKKKIL VYPLMLIHRV LSYNVIQLGS LTFFPKNIFI60
EKGITLS 67

- (2) INFORMATION ON SEQ ID NO. 174:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 56 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

LYHIIRKHSV DQHKWVHKNF FELGVCKHIC SFISVYKTVN QKDKTFFLVF VIFFLN 56

- (2) INFORMATION ON SEQ ID NO. 181:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 289 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

SRRTQGAAS RFPQFDITGQ DFSASAQRGG LVAHSOLDER AIEALKEFNE DGALAVLQQF 60
KDSDLSHWQN KSAFLCGVMK TYRQREKQGT KVADSSKSGPD EAKIKALLER TGYTLDVTTG120
QRKYGGPPPD SVYSGQQPSV GTEIFVGKIP RDLFEDELVP LFEKAGPIWD LRLMMDPLTG180
LNRGYAFVTF CTKEAAQEA V KLYNNHEIRS GKHGVCISV ANNRLEFVGS I PKSKTKEQIL240
EEFSKVTEGL TDVILYHQPD DKKNRGFCF LEYEDHKATA QARRRLIEW 289

(2) INFORMATION ON SEQ ID NO. 182:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

KLCTEWLKVIGIWRWVRGSC LGRLOFTWIR VGLREEIGV

39

(2) INFORMATION ON SEQ ID NO. 183:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

EAVMTLILIL HTYFLTQPYSP NPSEAKPSQT APSPSPYPF NL

42

(2) INFORMATION ON SEQ ID NO. 184:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

PSFSFYTPIS SRNPTLIQVK QSLPRQLPLI HLHIPPTFNH SVHNFYSLHT SYLLIFLTNKG60

(2) INFORMATION ON SEQ ID NO. 188:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 46 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

RSRFHMMLTL RALQLSLPTK IGGACFRVSR LSPTEKKKKK MSLEEA

46

(2) INFORMATION ON SEQ ID NO. 189:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 65 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ITFSHDAHAQ GASIIPPHKD RWRVFQGLSS LSYRKEKEKN VIRRGVTRQS VPRFVFPGVA60
ERDQF

65

(2) INFORMATION ON SEQ ID NO. 190:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

ECREAGPLFL QSRLELISFG HSRKHKPGDG LTCYASSNDI FFFFSVGER RETLKHAPPI60
 FVGRDN 66

(2) INFORMATION ON SEQ ID NO. 191:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

RQTEGETEML RKPSYTTLPR NTSLRECKKY YWRWKSARKTA MGRPRPGD

48

(2) INFORMATION ON SEQ ID NO. 192:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

RAETRSQGQL NEDKLGKLR CLESPAIQLY PEILPLGNVK STTGDGRAEK QLWAEQGQVI60

(2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

SCIAGLSKHL SFFFSLSLS CPWLRVSALQ LLPLRAFPFA SDLL

44

(2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

EIMNGLVLDN IWFHKLITSV LGESHFVNHT SEIYMLNGE QRRSCCKRCI KYLCCFCMRL60
RSFSLSPLE PIRISREAKL FCGFGNGHFP GKCIWIDD

98

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 115 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

AHSSTKAKSK SEFLPILPLC NTLRSSHNCF TPHLPVSCCT KSPSLSSFYR IVRQGRRALR 60
 RRAFEALSTL PASVKMRLHY SPEKRARFSH RSRCIFPGND HSQTHRTVWL LWISL 115

(2) INFORMATION ON SEQ ID NO. 196:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

SGVKRISCVL ETKAYCHCFK KSLCEMKKNM TNTGSHTYTY IQRNLTCTH TGRYRHTVPP 60
 KRSPNQSSYR FYHSVILSEV PTTAQLHTYP FPAAQSLLS HLFDTSSGRA EGHYAAEHSR120
 LSAHCQPA 128

(2) INFORMATION ON SEQ ID NO. 200:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

RPGVEPPLLRLRPDSETQKR VQGWGEMWSE GRFAFEKGSS RTHWDIVTHL NHLLIERCWP60
 PNNGRSGPGP RA 72

(2) INFORMATION ON SEQ ID NO. 201:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 77 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

GPSPYARGPG PDLPLLGGQH LSIRRWFKCV TMSQCVLELP FSNANLPSLH ISPHFWTRFC60
 VSESGNLLKR GGSTPGL 77

(2) INFORMATION ON SEQ ID NO. 202:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 60 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

EANTFLSEDG SNVLQCPVSF SNFLSQMQTF PHSTSLPIPG FVSVSLSQAT FSKEGVPLPA60

(2) INFORMATION ON SEQ ID NO. 203:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

PTTTLVIPLF FLSSRRKRQK DSFQTALCSL HCSFPAQAAS TGKAHVVTYPY FSEVLLFHGV60
 TLLSESKFRK QVLPLADKNH TSFL

84

(2) INFORMATION ON SEQ ID NO. 204:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

CDRVPLFLSY WCAVADSWLT ASSVSHVKG I LSPQPTCAP PGPANCFNF FFFFFFFLVET 60
 GSPSVAQDGL ELLGSSNPPT LASQSAEITG MSHYAQFEQD DLNLINSTPK QQLSLSQGCQ120
 GGLCEGKD

128

(2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

WVAGRRHLLS VQTKSLQVLG LDLCVTPESQ CIRLYYKLV WFLSAKGKTC FLNLLSDNKV60
 TPWKRTSEK YGVTTWAFPV LAACFGKLQC RLQRAV 96

(2) INFORMATION ON SEQ ID NO. 206:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

PDFRGFAGPA MFSRGFQVGR GERQGENAPC RGVQRSPASC PAVGWTSOL

49

(2) INFORMATION ON SEQ ID NO. 207:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

QISGVLAPR CFPEVFKWEE ESDKVKMPRA GASSGVLPAV RRWGGRLIYE GAHPPI

56

(2) INFORMATION ON SEQ ID NO. 208:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 68 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

CCSCQSSQVR YSDRMMGTFI NQTSTPPPD S WQDSAGRP GT GHFHLVALL F PLENLWKTSR60
 GPQNFGNL 68

(2) INFORMATION ON SEQ ID NO. 209:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 164 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

WGGRTLASAV SIPLRKCHSH RPTVLARKQP QSGVPPPYTA IASPDASGIP VINCRVCQSL 60
 INLDGKLLHQH VVKCTVCNEA TPIKNPPTGK KYVRCPCNCL LICKDTSRRI GCPRPNCRR1120
 INLGPVMLIS EGTSSACIA QSQPEGYKGR VLGHGWGTHS LWDG 164

(2) INFORMATION ON SEQ ID NO. 210:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 218 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```
SSAVPDGAVG  RPVAVAVGGP  PHSCRCRPCC  LMAAIGVHLG  CTSACVAVYK  DGRAGVVAND  60
AGDRVTPAVV  AISENEEIVG  LAAKQSRIRN  ISNTVMKVKG  ILGRSSSDPQ  AQKYIAESKC120
LVIEKNGKLR  YEIDTGEETK  FVNPEDVARL  IFSKMKETAH  SVLGSDANDV  VITVPFDGFE180
KQKNALGEAA  RAAGFNVLRL  IHEPSAALLA  YGVGQDSF  218
```

(2) INFORMATION ON SEQ ID NO. 211:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 186 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```
RKWTLTSMQ  KRMLKRPDNK  LKYVTKWQRT  AKQITHPFSS  NSTMSSMNIT  ILTSPSSSRK  60
YKRAEERRIV  RMGESMKTYA  EVDRQVIPII  GKCLDGIVKA  AESIDQKNDS  QLVIEAYKSG120
FEPFGDIEFE  DYTQPMKRTV  SDNSLSNSRG  EGKPDCLKFGG  KSKGKLWPF  KKNKMLSLT180
GGPFSS  186
```

(2) INFORMATION ON SEQ ID NO. 212:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

ISGRRVSLNF VSEFSITEFC PCWCLGYRPD GPGSFSPSCSG LEVSPLHFLK ACVQCSPKSI60

(2) INFORMATION ON SEQ ID NO. 213:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 68 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

DLCSTLSATK GSITCFLNKA LVSPPASSGL HYSETNSTSF AGGITVPISR LGPALQTSFG60
LLVLLTLL 68

(2) INFORMATION ON SEQ ID NO. 214:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 54 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

TISFFKSKRG LKQEGTGTS QMDLGEHCTQ ALRKCKGLTS RPEQDGKLPF PSG

(2) INFORMATION ON SEQ ID NO. 215:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 276 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

```

LPTAFLLSSV FWIFMTWEL FFPDLAGAPF YFSFIFSIVA FLYFFYKTTA TDPGFTKASE 60
EEKKVNIIIT AETGSLDERT FCTSLIRKP LRSLLHCHVCN CCVARYDQHC LWTGRCIGFGI20
NHHYYIFFLF FLSMVCGWII YGSFIYLSH CATTFKEDGL WTYLNQIVAC SPWVLYILML180
ATFHFSWSTF LLLNQLQIA FLGLTSHERI SLQKQSKHMK QTLSLRKTFY NLGFMQNLD240
FFQCQCGFLV KPCVVDWTSQ YTMVFHPARE KVLRSV                               276

```

(2) INFORMATION ON SEQ ID NO. 216:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

```

SPSRSPVVFA GEFLFKHPFV EESLMSFFHP DLHLMNPKAI STQFLYSVF

```

49

(2) INFORMATION ON SEQ ID NO. 217:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

KEINNYIRKE KNFKYLQFST PNHQDRWVQ KNAPEWF

37

(2) INFORMATION ON SEQ ID NO. 218:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

KFSSKDDRTS RRRSIIISER KKILSIYNPL LLITPKIGGS RKMHLGFTEE RS

52

(2) INFORMATION ON SEQ ID NO. 219:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

DKRNGIISK LSPEKTLKS ILKRKGTSDI SDESDDIEIS SKSRVRKRAS SLRFKRIKET 60
 KKELHNSPKT MNKTNQVYAA NEDHNSQFID DYSSSDSELS VSHFSFSKQS HRPRTIRDRT120
 SFSSKLPSHN KKNSTFIPRK PMKCSNEESC

150

(2) INFORMATION ON SEQ ID NO. 220:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

NKWNKSKLGK EISKATQSLD PAQLADPCHS LAVAASLCSL KGEFGQCFFS PWAWSLHSGK60
 QTSGPFPEKSQ ECLAAWVILI AMF 83

(2) INFORMATION ON SEQ ID NO. 221:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

NSKLVDCRM E TWLLRRHWVSF SLCVSCWGVV MIVSALTHCT RWQQDTALHK MAAPLQLFPQ60
 PPSLHPHFRFG LWFLSSVTYC LRS 83

(2) INFORMATION ON SEQ ID NO. 222:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

CLHNREPDIF RILSSSYGI LRPRSYLQTK WPWSLQNIAM STHQARHSW DLGKGPLVCF60
PLCSDQAQGL GKHWPGSPFS EHREATARE 90

(2) INFORMATION ON SEQ ID NO. 223:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 114 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

QSLRHCWLNI SLQRDGAFFE PGAGPVSSKA LDVFLVTRRR GCQMPLKPSG LVWPRAAGQG 60
RAEKWSSSQL ALPSPTQPRP RWSLDSILTS ASPKVQMSKC LVVQSQEMGS YLKS 114

(2) INFORMATION ON SEQ ID NO. 224:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 145 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

GCVGGGRAEA MAEKFHLEE HLEKFVENIR QLGLIIVSDFQ PSSQAGLNQK LNFIVTGLQD 60
IDKCRQQLHD ITVPLEVFEY IDQGRNPQLY TRECLERALA KNEQVKGKID TMKKFKSLLI120
QELSKVFPED MAKYRSIRGE DHFPS 145

(2) INFORMATION ON SEQ ID NO. 225:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

QGTMRTEGLR GVSRAQSHLS RKVASALAVP ASRRIAVPGD LHTGRVSWLR RRVILPPDAS60
ILSHVFRKYF RKFLNQAFK FLHGVDLAFN LLIFS 95

(2) INFORMATION ON SEQ ID NO. 226:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

ALRPPLYALG QQVGAVTGPA DCSATAPLDF WIFWKQSQNS GLLGGWQRGM VRGPPFISLF60
SIRWQSTGHP WWVSGPRPMP TLPFESR 87

(2) INFORMATION ON SEQ ID NO. 227:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

APALATQPPL SLPRGTGPAY LNSLTMLQT WLLDSKLLSS NVLLPHFHL HICLLLYWFL60
LLNLYFHSWV LCLPFFFS A 79

(2) INFORMATION ON SEQ ID NO. 228:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 87 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

RSMSVEASFV CLGTTGRCCCH WSCRFSNSP FGFLDILETK SEQWPTGGLA EGYGKRTSFH60
LPVQHMAVH RSSLVGVPRK THAHLTL 87

(2) INFORMATION ON SEQ ID NO. 229:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 150 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ATLSRFFGRI FNLALTQVFP FLFSSPNDKK SFCISIEGEWN GVMYAKYATG ENTVEVDTKK 60
LPIIKKKVRK LEDQNEYESR SLWKDVTENL KIRDIDAATE AKHRLEERQR AEARERKEKE120
IQWETRLFHE DGECWVYDEP LLKRLGAAKH 150

(2) INFORMATION ON SEQ ID NO. 233:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 206 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

DSLRRGLGIC LWEFIHLSLL FTSPKPGFPL LKPAVISQLE GGSELGGSSP LAAGTGLQGS 60
 QTDIQTNDNL TKEMYEGKEN VSFELQRDFS QETDFSEASL LEKQQEVHSA GNKKKESNT120
 IDGTVKDETS PVEECFFSQS SNSYQCHTIT GEQPSGCTGL GKSISFDTKL VKHEITNSEE180
 RPFKCEELVE PFRCDQLIQ PSREQH 206

(2) INFORMATION ON SEQ ID NO. 237:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

RIRRSALIFS KGVQRWRRVF GRRVSPGSGN TESEASDYRK KQGTSKVFGR RVLKKIQ 57

(2) INFORMATION ON SEQ ID NO. 238:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

GTLLFTVVTG FALCVPAAGT YPSENPPPS LYLTKDQCR TPDF

44

(2) INFORMATION ON SEQ ID NO. 239:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 74 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

NLYPTLEFNP SHEVVELTGF FSTPFFRTPL RYLVFYGSHW LRSLCSRCRD LPAFRKPAAI60
SVHPWKRSVQ NAGS

74

(2) INFORMATION ON SEQ ID NO. 243:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 183 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

AAVAFGAKGT SPAEARSSRG IEEAGPRAHG RAGREPERRR SRQQRGGGLQ ARRSTLLKTC 60
ARARATAPGA MKMVAPWTRF YNSCCLOCH VRTGILLGV WYLIINAVVL LILLSALADP120
DQYNFSSSEL GGDFFEMDDA NMCIATAISL LMILICAMAT YGAYKQRAAG SSHSSVTRSL180
TLF

183

(2) INFORMATION ON SEQ ID NO. 244:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 157 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

QQHVVHCHCDF SSHDPDMCYG YLRVQVQATRS WIIPFFCYQI FDFALNMLVA ITVLIYPNSI 60
 QEYIRQLPPN FPYRDDVMSV NPTCLVLIIL LFISIILTFK GYLISCVWNC YRYINGRNSI120
 DVLVYVTSND TTVLLPPYDD ATVNGAAKEP PPPYVSA 157

(2) INFORMATION ON SEQ ID NO. 251:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

ATKTVPRQRW SPPHCPRPNP SLNLLRCGWG NRGKTEAPDA FSLLCSSAID CPDVQRETHT60
 RFAHENWGAD GQADRLCLFS E 81

(2) INFORMATION ON SEQ ID NO. 252:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GVDGETEAKL RHLMSACCA AVPLTALMFR EKRTQGLPMR IGEQMAKQIG YVCFLSDEVR60
KPCGSGGHLW FILFFYPWLL EMVTFRVQL HlseHYC 97

(2) INFORMATION ON SEQ ID NO. 253:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 114 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

LEILGIFSRV SKLSSSPDT HPSSQIGVAI LGGRVVYGTG GCLHISQNYF RTIVPKSRVF 60
TGRQNLFSMP VPQLLSQIPI LGSHQLPIPH QTATVPSLSP YCSFKSCSQE RNCH 114

(2) INFORMATION ON SEQ ID NO. 254:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 53 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

IPSPQGPFCR SYSDPRKCPF PIVVLCLWGL VYPRGNCGEI IGLRVKRALV LEL

(2) INFORMATION ON SEQ ID NO. 255:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

QVDTIISTRK GLKLQNQC SL DSQTNDFTV TPGID

35

(2) INFORMATION ON SEQ ID NO. 256:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

TKPQRHRTTM GKGHFLGSEY DLQNGPCGLG IYPYAVFWSN A

41

(2) INFORMATION ON SEQ ID NO. 260:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 205 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

GSVKVPASPR PGGTSLGPFV AAKELSFSPR NGRRGQLPRP PGS�TLLLF SSASRGSPAS 60
LSPGGIRLLL PPPPHLLPGQ PACPAAVMCD KEFMWALKNG DLDEVKDYVA KGEDVNRTLE120
GGRKPLHYAA DCGQLEILEF LLLKGADINA PDKHHTPLL SAVYEGHVSC VKLLLSKGAD180
KTVKGPDLT AFEATDNQAI KALLQ 205

(2) INFORMATION ON SEQ ID NO. 264:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 180 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

RNMSSFSRAP QQWATFARIW YLLDGKMQPF GKLAAMASIR LQGLHKPVYH ALSDCGDHV 60
IMNTRHIAFS GNKWEQKVYS SHTGYPGGFR QVTAAQLHLR DFVAIVKLAI YGMLPKNLHR120
RTMMERLHLF PDEYIPEDIL KNLVEELPQP RKIPKRLDEY TQEEIDAFPR LWTPPEDYRL180

(2) INFORMATION ON SEQ ID NO. 265:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 78 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

VIGYPSRINS EPSPIYINRP GNNVKLNCMA MGISKADITW ELTDKSHLKA GVQARLYGNR60
FLQPQGSMTS SACHKEGW 78

(2) INFORMATION ON SEQ ID NO. 266:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

ATPLCGMLNG SLIPGVEEIC FHTDEPEPLP SDATYPLTPT

40

(2) INFORMATION ON SEQ ID NO. 267:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

VGIWQEDHLP QSLGFLNKKE IVFLSWLLRL LKLALPLKYD ISFAVLNLKL VASSVAHFQF 60
 LYQASLLSFP LRMGQVCSGG HSVRFSRGFG RGFKGKYS GG RMGSGVKVGD KGGRAKGGVE120
 GWGPLYLDRGM FGGQGGK

176

(2) INFORMATION ON SEQ ID NO. 268:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

LVYFKQGTKE PGKRSGHVKR DTQDTLRDQS GSTPVLLPEC LCVNFCFLQN KRQQRKLLNQ60
 NTDPMRNGAC FCDPGLSAR LQELTDGQLL IF 92

(2) INFORMATION ON SEQ ID NO. 269:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

NLVYTMWLQI YVNVHFEHIY VLNKEMLVTK IRFTLKEEF YSKHSNLFK CFKIQSIVFK 60
 VAVKASTYVK TQKEGSSDRN TAPLLCCFSC SLYTLKHLL SGA 103

(2) INFORMATION ON SEQ ID NO. 270:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

FIYQSKVRD IFAVTLAILS LQSPTSRVQC TSNNSLKTRH LTISVYLCK VNKSSIIKE60
 LCFYQRLSPS EFLHKLMPSL QL 82

(2) INFORMATION ON SEQ ID NO. 274:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

QQHHLPQSLG FLNKKVVVEL TWLLRLKLKLA LPLKYDISFA VLNLKLVASS VEHFQFLYQA60
 SLLSFPIRMD MCCSACHVCN ASCREFGHSI KEKIQ 95

(2) INFORMATION ON SEQ ID NO. 275:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

LLRQYHTSSF YTKPVSSVFP LEWTCVQRV MSVMLHAESL VIVLKRKYSE VTMSPE 56

(2) INFORMATION ON SEQ ID NO. 276:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

HAEQHMSILM GKLRLRLAWYR NWKCGTDEAT NFKFRTAKLM SYFKGRANFN NLNNQVKNTT60
SFLLRNPND 69

(2) INFORMATION ON SEQ ID NO. 277:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 95 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

YILEISPLKP SLAPTSGLM PQGFPPHECN PRYPSLSTPS QTPTPGIARE DFGLANCVGY60
VSVVLIRDVH DCQSAFLTSV TTLRCNSSQ KKTFS 95

(2) INFORMATION ON SEQ ID NO. 278:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 133 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

PTQFARPKSS RAIPGVGVWD GVDNEGVLGL QKWGGNFWGI SPQEVGASDG FRGDISNIYQ 60
PWALSPCCSQ HGPHTSSLRL TWELVRNAGS PRSIELEAVL TRSPVIFMAQ SSFLRDRCLL120
LSAGMRHPWG RCG 133

(2) INFORMATION ON SEQ ID NO. 279:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

LKQHSNQHNN LLGQSLHGQS LGWESGMGWI MKDTWGCRCRG VGIPGASVHR RWGPAMASGV 60
 IFPIYISPGH SRPAAHSMVL TPAASALPGS LLEMQDLPLD LS 102

(2) INFORMATION ON SEQ ID NO. 283:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

VYSANEGQNF QFIDGYSAAD ESLCVSHFNF CKQRHRPRTV RGRTSFSSKL PRHNKENSTF60
 ISRKPMECNSN EEVNVNQGSD GSMGKF 86

(2) INFORMATION ON SEQ ID NO. 284:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

GAEIVFLQNC LGIIRKIALI FQGNRWNVQM RKLLIKSRM DQWVNFWRQ GGAYIHSNPD60
VIWSGGQWK 69

(2) INFORMATION ON SEQ ID NO. 285:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 59 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

LTSSFEHSI GFLEIKVLFS LLCLGNFEK LVLPLTVLGL CLCLQKLKWL THKLSSAAE 59

(2) INFORMATION ON SEQ ID NO. 286:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 65 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

GKEPQPESNS IMVKFPTSS CEWVIRKNE PDKNQRQMG SVTGSLSL NPIEYCGLT60
CQGGD 65

(2) INFORMATION ON SEQ ID NO. 287:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

FLSFGSSFFL ITHSQDMSGV NLTMIELLSG WGSFPHRKDI LKTKKYLN

48

(2) INFORMATION ON SEQ ID NO. 288:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

ARNIQSDLEW MIKIQSQTPS VFDFCLLDPH FS

32

(2) INFORMATION ON SEQ ID NO. 292:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CAKLETGDFD LSYLFAFCAS PSNLVHLSSH SCYFQVKQDI LGVKSLWVFC FYVYKNGFCV60
 PEPCKYQLIW KLTIIM 76

(2) INFORMATION ON SEQ ID NO. 293:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

VELSLLFPQL SQLLVNFKEA GHDDSHLLSQ NFGRRRWADS LSPGVQDEPG QYGPTSSLTK60
 HPH 63

(2) INFORMATION ON SEQ ID NO. 294:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

PPKCLVSLFN NMNETKDEPD YLVTHRRRTS SSGNQILFQA WHIKGKKGSE RRVRYHLKPF60
 QKIWQKTASK SIR 73

(2) INFORMATION ON SEQ ID NO. 298:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

PLGPASSAFG FSGSKSRSEE GRDGTASPGT FKYHPWSPLS SLREWTSQST SSGLSDLLLC 60
 LYQPWQGSRI HLVGSGGPSQY HWGSNKFLEP QSLGPGSQLI GDGVVFQARA EFGTSGHELE120
 GNSVSYELGP WP 132

(2) INFORMATION ON SEQ ID NO. 299:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

ESRRGALAGP LSKAGEGRPG WYLNVPGLMS HPFLPHSYSL TLMKARADAG PKGKNVLSVF60
 SGFYSLVSLH 70

(2) INFORMATION ON SEQ ID NO. 300:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

GVKAREYRED VFTFRACVSG FGHQQRVGV RKEGMGQHPW DVQVPSWSFF SSLREWTSQS 60
 TSSGLSDLLL CLYQFWQSSR IHLVSGGFSQ YHWGSNKFLF PQSLGPGSQL IADGVPFKLVI20
 PARAEFGTSL KGNSTVYELG PWP 143

(2) INFORMATION ON SEQ ID NO. 304:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 408 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

FANWEFMGTE QLQPQLPSFK VWSRCRCRQG PTKFNQVSRM QTPAPVSRRV GLAVSLTPPP 60
 SGQSGPSVMG KAAACPATPA SAPSQGLSFG GPVSCWPGSP LLHLIGGRQL LDLCPCGGRS120
 LPFSSSSSSS VNSDSAPDGP RGLGCFGGVV LGGRGFKYLL YFLFVAATQQ ILLGRASAF180
 LKRDVGDPDV VAPAFFAVAG HLHQAVALPG VRVRVRDQET MQVSGLGGAL GLGRLSQELR240
 QALHARHPHD VDVVVTAEGE DEREVDLQGD VILLLLVNGQ EAEDHAVVWH IHQLGRLVHP300
 HCEAILALSG HQKLLHRGGH RLHLRRVVA RHELFQRHVA IIIHSGCGST AVPREKLQNP360
 SQRAQNLPTF LERSKTEFGK QRNFSRKGGK IYCKVLGEDN PGSCGNQR 408

(2) INFORMATION ON SEQ ID NO. 305:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 169 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GWGVWQAGLD PVLGPPSSAV PSLLLGVVSM VWPHLQLCLS AVPLASSSLN SAANSPVSSR 60
 ARQGWWGWCW QQLLSWCDLS GLHLRGRNGP GYRQIHPGW SPRPPGLGAA GGRWLLVGRW120
 PSCLACLPCL SSSPNALSVS AFLAPGLSTP SAYKAVSPFQ TTVWLQPIR 169

(2) INFORMATION ON SEQ ID NO. 306:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 120 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

ILQLGHQFPL VPARAGAVGV GSSFSLGATF PASTSEVGMG QAIEVRFIQA GVLVLRAWGL 60
 LGGAGCWWEG GHRAWLVFPA SLLLLTLCLS LLSWPRASPL PQLIRLCLLL RPQSGSSPSG120

(2) INFORMATION ON SEQ ID NO. 307:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 472 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

SESLTHPGEE PGGFFPGGAP TMATPLVAGP AALRFAAAAA WQVVRGRCVE HFPRVLEFLR 60
 SLRAVAPGLV RYRHHRLCM GLKAKVVVEL ILQGRPWAQV LKALNHHFPE SGPIVRDPKA120
 TKQDLRKILE AQETFFYQQVK QLSEAPVDLA SKLQELEQEY GEFFLAAMEK LLFEYLCQLE180
 KALPTPQAQQ LQDVLSWMQF GVSITSSLAW RQYGVDMGWL LPECSVTDSV NLAEPMEQNF240
 PQQRLALHN PLPKAKPGTH LPQGFSSRTH FEFLAGRHFN LAPLGRRRVQ SQWASTRGGH300
 KERPTVLMFF FRNLGSPTQV ISKPESKEEH AIYTADLAMG TRAASTGKSK SPCQTLGGRA360
 LKENFVDLPA TEQENCLDC YMDPLRLSL PPRARKFVCP PSLCSSLVITI GDLVLDSDDE420
 ENGQGEKES LENYQTKTFD TLIPTLCEYL PPSGHGAIPV SSCDCRSDSSR PL 472

(2) INFORMATION ON SEQ ID NO. 308:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 138 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

PGFALRGAIG PREGRGGGRG YRRSSGRQPL VSWQRQARCG SGGAMSFCSF FGGEVFQNH 60
 EPGVYVCAKC GYELFSSRSK YAHSSPWPAF TETIHADSV KPEHNRSEA LKVSCKGCN120
 GLGHEFLNDG PKFGQSRF 138

(2) INFORMATION ON SEQ ID NO. 309:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 121 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

SYGATAAFLS RSEASYFRTD CETGFRFLPS WTRGQGCAPS ACLPSRSQTI PTLAGLEGFD 60
 QSGSCSDQGG GSWQGRPPFF FCLLSSLDGV GLSFGEDSL SWNWSAQGRV QRQGGQKKVR120
 V 121

(2) INFORMATION ON SEQ ID NO. 310:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 249 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

SEQGAKSADS VAAQPRPVPA EGMNHQQMSL FSKKRKGLVQ SRGLGSVLMF QPLRPAFLSR 64
 RPFQQLQGGM ANVWFQCGGR LGWVWAARLV TLGGRSFFAF RDKLQRAAEY SESGLPRLGA120
 VVQELVAQPI ATLATGHLQG FRSIVLRTLQ HAVGVNGLGE RRPWRRVCIL RAAGEQLIAT180
 LGTHVNARFK VILENLAPEE AAERHGATGT AARLPLPTDQ RLPTRRPPVP ASTSPPLPRT240
 NRSPEGESR 249

(2) INFORMATION ON SEQ ID NO. 311:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 204 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

LGSSWIFVNL TVRFCILGKE SFYDTFHTVA DMFYFCQMLA VVETINAAG VTTSPVLPSL 60

IQLLGRNFIL FIIFGTMEEM QNKAVVFEVF YLWSAIEIFR YSFYMLTCID MDWKVLTWLR120
 YTLWIPLYPL GCIAEAVSVI QSPIFNETG RFSFTLPYPV KIKVRFSFFL QIYLMIFLGI180
 LYINFRLHYK QRRRRYGQKK KXIH 204

(2) INFORMATION ON SEQ ID NO. 312:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 155 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

RISGCSRSS CCFQCPTADR FKKPTEQQQN EVFLRSIQKC TVPPLTRTST QVNGLSQCRR 60
WKAAIFYVCA QPYSLEVCLA YSNISLSKA VHCYCQFDLH TVFPLDPCYH LDLVCVCVYV120
CLCVCGLVWF ETGSCTVTGP CSAVAQSRLT AALT 155

(2) INFORMATION ON SEQ ID NO. 313:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 70 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

AVMDQVMQFV EPSRQFVKDS IRLVKRCTKP DRKEFQKIAM ATAIGFAIMG FIGFFVKLIH60
IPINNIIVGG 70

(2) INFORMATION ON SEQ ID NO. 314:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 112 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

FRNRKHLERK KKNPQNIQAN LYSVSFSHPH TCSPISKMKN SLPKCIQPPT MMLLIGIWIN 60
 FTKKPMNPPII ANPIAVAMAI FWNSFLSGLV HLLTSRMESF TNCRLGSTNC IT 112

(2) INFORMATION ON SEQ ID NO. 315:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 110 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

DEKLSSKMYs ATNNDVINRN MDQFHKEANE SHYSKSYCCC HGNLLEFFSI RFSASFNQPN 60
 GVLYKLPTWL NKLHYLIHDC LPNRHLKCQG HVALELADGG PPEPESGFLP 110

(2) INFORMATION ON SEQ ID NO. 316:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 113 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

GSSEGSYSsQ TETCPLTPSL VTGSMFAQNF LRGLSLQKSN LLPECCCLASE NLTLsFFPSVN 60
 GHRcVAQGSSE TSesRAQWHG VALWVRKVIG QLYCKRANKYV VQFCCKQVCS VVL 113

(2) INFORMATION ON SEQ ID NO. 317:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

GKRGQLWSLN LLAPCAGYKT RSWSKIALTP NPNVQDLGA TQPVVWCWF PFFVCLLVSK 60
 IALLGTAWKV QAFLLARSGL ASSPCLHSVP KEDFCSTLWS 100

(2) INFORMATION ON SEQ ID NO. 318:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

SQIISNLVDN YSIQELMFSE TVINRIFTSG LAGRLGGRKG RVEGWVAHQN GDEPGKTTML 60
 LFLYPLKPIS RVLNDAFFVC FLIGSQISFS IKNWGYPKE T 101

(2) INFORMATION ON SEQ ID NO. 319:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 368 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

WWRLNKSAS VRQQAADLIS RTAVVMKTCQ EEKLMGHLGV VLYEYLGEED PEVLGSILGA 60
LKAIVNVIGM HKMTPPIKDL LPRLTPILKN RHEKVQENCI DLVGRIADRG AEYVSAREWM120
RICFELLELL KAHKKAIRRA TVNTFGYIAK AIGPHDVLAT LLNNLKVQER QNRVCTTVAIL80
AIVAEATCSFF TVLSPALMNEY RVPELNVQNG VLKSLSLFE YIGEMGKDYI YAVTPLLEDA240
LMDRDLVHRQ TASAVVQHMS LGVYGFQCED SLNHLLNVVW PNVFETSPHV IQAVMGALEG300
LRVAIGPCRM LQYCLQGLFH PARKVRDVVW KIYNSIYIGS QDALIAHYPR IYNDDKNHLI360
IRLMNLGL 368

(2) INFORMATION ON SEQ ID NO. 320:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 121 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

YPFFTLQQRN RVFDISSYVK EMLQNVNCFK LKLEPLKRPY IYLIVYIMFN ICQSILQVCS 60
FISIKYGYVY AQLLKWYICV YICTPNNIVC TFCFLYCICA GFFRLYQCNL CLLRYVQKMS120
I 121

(2) INFORMATION ON SEQ ID NO. 321:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 114 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

FFFFFFFF HSNVYFFFF FFFFFGKNVI YLHCFHSSTV VLGLNISITL LPPIYILLEY 60
 YYKYNIQFKK TYGETQLMFF SPLYALLSII RLQWKFIWTF SVHILAGRDT TDKA 114

(2) INFORMATION ON SEQ ID NO. 322:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 597 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

EKCGQYIQKG YSKLKIYNCE LENVAEFLGL TDFSDFKLY RGKSDENEDP SVVGEFKGSF 60
 RIYELPDDPS VPAPPRQFRE LPDSVPQECT VRIYIVRGLE LQFQDNNGLC DPYIKITLGK120
 KVIEDRDHYI PNTLNPVFEGR MYELSCYLPO EKDLKISYVD YDTFTTRDEKV GETIIDLENR180
 FLSRFGSHCG IPPEYCVSGV NTRWDQLRPT QLLQNVAREK GFPPQILSED GSRIRYGGRD240
 YSLDEFEANK ILHQHLGAPE ERLALHILRT QGLVPEHVET RTLHSTFQPN ISQGKLQMWV300
 DVFPKSLGPP GPPFNITPRK AKKYILRVII WNTKDVLDE KSIITGEEMSD IYVKGWIPGN360
 EENKQKTDVH YRSLDGEENF NWRVFPFDY LPAEQLCIVA KKEHFWSDIQ TEFRIPPRLI420
 IQIWDNDKFS LDDYLGFLLEL DLRHTIIPAK SPEKCRDLM PDLKAMNPLK AKTASLFEQK480
 SMKGWGPCYA EKDGARVMAG KVEMTLEILN EKEADERPAG KGRDEPNMNP KLDLPNRPET540
 SFLWFTNPCK TMKFIVWRRF KWVIIGLLFL LILLLEVAVL LYSLPNYLSM KIVKPNV 597

(2) INFORMATION ON SEQ ID NO. 323:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 76 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

IRRDKAYLTF KWRDDENPLI QSFRTKRQSS DKSMTWMKCP TGALDIFNFC DYVKEVDFD60

NGAEANISKR NPNFFP

76

(2) INFORMATION ON SEQ ID NO. 324:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 90 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

FFLYSFSSDN HDFSFKTIY LAFVSGGELA 'SILKPAIIV NLRTGLSWGSG EGKELFEQMC60
VGGTGFHPTA KLVLLLEISFY NTKISLCQRF 90

(2) INFORMATION ON SEQ ID NO. 325:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 60 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

TRSLLYFHMV LILWEEVGIP FTVNGFCSII CKVHLFHIIA EIKDVQGPCR AFHPCHTLIR60

(2) INFORMATION ON SEQ ID NO. 326:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 42 amino acids

(B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

IRNEKKGCVL SVGEMELVLV VLEQDRHLVL MLWSFVIVEH RG

42

(2) INFORMATION ON SEQ ID NO. 327:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 50 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

ATCSDNRSKI FQLFNLECYV LLEPAICMYR INNFYSGQV ILRQSQWIK

50

(2) INFORMATION ON SEQ ID NO. 328:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 48 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

PKGVVVNPGA LLSQRTTASE LSACPAPTLP GPVPSHLLIR HSLSSHSL

48

(2) INFORMATION ON SEQ ID NO. 329:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

ISEVAVNFSV LLLASVCLPI DTHYTNVPSK CSLHICFHCV PTGAMKCVRS PSSGGMSAAL 60
TTAIRIVLCG IFIYINFICT VISLFICQVT ICKSYTHKLL 100

(2) INFORMATION ON SEQ ID NO. 330:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

EAQKWDCIWT KNYKKVQSLV SRMQALALGD GSSLENAAAD SLFQRRSFER RVCYISFFT 60
TLWRLKDLVV SCFLKITGIW RPKPFEWTDI SSKYFFIKVF EGDGDFDLWL DILGFDPDYIV 120
LS 122

(2) INFORMATION ON SEQ ID NO. 331:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

ENWASRYFQS SFTEQKVWVG HWLEGDSP TL TVTIWAATGG IVQLASRCIP HLKVCWIKAI 60
 YTLAKSKAKE IALDPESQQD HLIFPNQHLG QQLPSTFLFH SWFFFFFLLQ DLAVTQDGVQ120
 WHDH 124

(2) INFORMATION ON SEQ ID NO. 332:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

LNVDLLITRR LCEKIYVYIY MICRSHFFYQ ALFSLQSHSL TVCNSWFMLM IDKYPVEVTF60
 SNYHCNDNLS HVTYCNFLAS FP 82

(2) INFORMATION ON SEQ ID NO. 333:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

RLVKYKNSLN REKASQVFPL KVKYGTGFHN KVNDFKNLTF FRRKKKTSYE PSLVNLHVYK60
IFPLFKKCFK KILRSHEIMP WS 82

(2) INFORMATION ON SEQ ID NO. 334:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 75 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

KLEYIMSTAN CSFCLILTDY AFPQRSSRSR IYRHIYSGSL KEKILSSIM IYHCAINQKN60
QVRNTIKTTL KGKNF 75

(2) INFORMATION ON SEQ ID NO. 335:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 72 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

NEYCSWSTCI KQKTCQLLGA NTQNLVPVFF FFLTIVYTF LRIKFVTKSP MSFTCIYDHQ60
MVIRATYVNA CL 72

(2) INFORMATION ON SEQ ID NO. 336:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

THNTSTITAY RKLQSTLQAS KVHSVAQSPW RGRDLKVLMS SYFTCFLLST QCKMNFHSL60
YFRLKIDSFL VLTLTLEGTV VPGKRSRFTV PNH 93

(2) INFORMATION ON SEQ ID NO. 337:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

LGPRGEIEVY LAKSLAEKLY LCQYPVRPAS MTYDDIPHLS AKIKPKQKQV ELEMAIDTLN60
PNYCRSKGEQ IALNVDGACA DETSTYSSKL MDKQTECSS 99

(2) INFORMATION ON SEQ ID NO. 338:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

GKSRRSACPS ASRNTCWSRR RRPRPRSAQS APLCCGNSWG SGCWPSQAL PSAAWA 56

(2) INFORMATION ON SEQ ID NO. 339:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 59 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

GRAEGLLVHQ LRGIRAGLVG AGPVHVQRNL LPFAAAIVGV QGVDGHLKLY LLLGLDLG 59

(2) INFORMATION ON SEQ ID NO. 340:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 157 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

QPSSLLHHC PYPYPRHLLA TPLLKPQLLA GSPAHASLIS FLASPQRASR QHGGPSPQAG 60
TLSCPLVELG GSSGGRGLCH GSADPTNRAA EPQERGEPA GDRRLPEWG RVSLAESPGAL20
EFRCPGSLGE WGEIPEKESS AHPKTEEAAL CPAFGSH 157

(2) INFORMATION ON SEQ ID NO. 341:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 260 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

```

NSCWQGPQL MPASSPFLLA PKGPPGNMGG FVREPALSVA LWLSWGAALG AVACAMALLT 60
QQTELQSLRR EVSRLQGTGG PSQNGEGYPW QSLPEQSSDA LEAWESGERS RKRRAVLTQK120
QKKQHSVLHL VPINATSKDD SDVTEVMWQP ALRRGRGLQA QGYGVRIQDA GVVLLYSQVL180
EQDVTFTMQQ VVSREGQGRQ ETLFRICIRSM PSHFDRAVNS CYSAGVFHLH QGDILSVIIP240
RARAKLNLSP HGTFLGFVKL                                     260

```

(2) INFORMATION ON SEQ ID NO. 342:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 201 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

```

TPASWIRTPY PWACRPLPRL RAGCHITSVT SESSLEVALM GTRCRTECCF FCFWVSTALL 60
FRDLSPLSQA SRASELCSGR LCQGYPSPFW EGPPVPCSR L TSLRLC SSV CNVSRAMAQAL20
TAPRAAPQLN QRATESAGSL TGPPMLPGGP LGASKKGDEA GMSWGPCQQL WFQEWGSKV180
AGRVVRVAVV QKGRRLRKE K                                     201

```

(2) INFORMATION ON SEQ ID NO. 343:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 165 amino acids
- (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

GRRSRMEIPV FVQFSWLRRA SAPLPGLSAP GRLFDQRFGE GLLEAELAAL CPTTLAPYYL 60
RAPSVALPVA QVPTDPGHFS VLLDVKHESP ESIYKVVGE HVEVHARHEE RPDEHGEVAR120
EFHRRYRLPP GVDPAAVTSA LSPEGVLSIQ AAPASQAAPP PAAAK 165

(2) INFORMATION ON SEQ ID NO. 344:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 116 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TALAAQPQASQ AQSPHPNNVL DCTDLPLQTI QAWFPRPOPS PATRQSTTAP SSFFSAVKPQ 60
PATPDSGTLF RLPQLLDRF TRTENTKLYR LSHPNLRLC TDVLGFLPNS NQTFSF 116

(2) INFORMATION ON SEQ ID NO. 345:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 111 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

DIRAESGEVG VGESVQFGVG CSSWPGVQEL GQSKKGSRVW CGWLGFHGRK WAGGGSCRLS 60
 GCRGRIGSWE PGLDGLEWEV CAVQDVWVGW GLCLTGLGLG QGCLHNNLVS K 111

(2) INFORMATION ON SEQ ID NO. 346:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 53 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

RTEEEKKKKE KNQQFQLFTP KCWSFYVKGR IPGYGHGVYK YVGRFSANSE PTV 53

(2) INFORMATION ON SEQ ID NO. 347:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 51 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

NELKWTNRAE LSVGWQSWKP AFPASHQLNE VMSIQLRLF FRNNHAFLNP N 51

(2) INFORMATION ON SEQ ID NO. 348:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 150 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

RHAGGGALGN LPPQPPGSGV MHPETCPSTF LASPLPHSIA PGLFLDLFVL VLALFLIFFY 60
 YESPGRRGDS GSWPGPGRQV ALEMGKCLCR GAELSLCFSF FPLLLPLHTP VAGRNLGFPPE120
 SLGVPPFLPH FGGTPRAEGL FLLLESFWAV 150

(2) INFORMATION ON SEQ ID NO. 349:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 131 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

RSFLTRSVIK LPKRKRTRGET SPGPWAFLEPG GVRRVGPPSF QGSRGSFQPR GCEGEGVEEK 60
 RRNRERAQRL DDTFFSPGP PAVLAQASSH CHLCVQEIHN KKKSKTKPKP KQNPKGKDLG120
 QWNEEEGRGR R 131

(2) INFORMATION ON SEQ ID NO. 350:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 151 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

RKKGETEREL SASTQTLSHL QGHLPSWFRP APTVISASRR FLIKKNQKQS QNQNKIQKEK 60
 TWGNGMRKRG GEEGRAGLW MHSNRARGLG RKIPQRPAAC VALARHVVEG GRLPHPVEI120
 LVAGLLGGVK FVSDRQAGKG LGDGGGGRER V 151

(2) INFORMATION ON SEQ ID NO. 351:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

TLTAHEGRGG KCTEEGDASQ QEGCTLGSDP ICLSESQVSE EQEEMGGQSS AAQATASVNA 60
 EEIKVARIHE CQWVVEDAPN PDVLLSHKDD VKEGEGGQES FPPELPSEE 108

(2) INFORMATION ON SEQ ID NO. 352:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

KFFGNSLHAT PKCTPITLWL FSEKDFSQIV PFTPLRAALG NSPDHLLPFS RHLCVTAGHP60
 GLEHPPPTD THEYGLF 77

(2) INFORMATION ON SEQ ID NO. 353:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

TYSIHLHSQT KLKSLKVHKK IAQLKGAEYT QNCHPTVFSV FPAILFPFPQT SSAPSHPKYA 60
 IVFVILIKIL KQKFIVEQFM STKVCLSCSC PVICESSGFII QIKKILKNFL VTACMQPLSV120
 PL 122

(2) INFORMATION ON SEQ ID NO. 354:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 457 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

PVCEPLSCGS PPSVANAVAT GEAHTYESEV KLRCLEGYTM DTDITDTFTCQ KDGRWFFPERI 60
 SCSPKKCPLF ENITHILVHG DDFSVNRQVS VSCAEGYTFE GVNISVCQLD GTWEPPFSDEL120
 SCSPVSCGKP ESPEHGFVVG SKYTFESTII YQCEPGYELE GNRERVCQEN RQWSGGVAIC180
 KETRACETPLE FLNGKADIEN RTTGPNVVYS CNRGYSLEGP SEAHCTENGT WSHPVPLCKP240
 NPCPVFFVIP ENALLSEKEF YVDQNVSIKC REGFLLQGHG IITCNPDETW TQTSACKCEKI300
 SCGPFAHVEN AIARGVHYQY GDMITYSCYS GYMLEGFLRS VCLENGTWTS PPICRAVCRF360
 PCQNGGICQR PNACSCPEGW MGRLCCEPIC ILPCLNGGRC VAPYQCDCPP GWTGSRCHTA420
 VCQSPCLNGG KCVRPNRCHC LSSWTGHNCS RKRTGF 457

(2) INFORMATION ON SEQ ID NO. 355:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 210 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

GVRAASKEIE ELRRHREGT SRAVTGEGPA AGRMTVPKQT QTPOLLPEAL EAQVLPREFP 60
RVLQVQAQVQ SQTQPRIPST DTQVQPKLQK QAQTQTSPEH LVLQKQVQV QLQQAEPQK120
QVQFQVQQA HSQGPQVQL QQEAEPKQV QPQVQQAHF TAPRAGAAAA EEAGPDTDFS180
TGAHTGHSQA SRHRELLPGA VFSFRPPGAG 210

(2) INFORMATION ON SEQ ID NO. 356:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 292 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GRAGRATMF SQQQQQQLQQ QQQQLQQQLQ QQLQQQLQQ QLLQLQLQLL QQSPPQARCH 60
GVSGGGPPQPF QQPLLNLQGT NSASLLNGSM RQRALLQLQL QGLDQFAMPP ATYDTAGLTM120
PTATLGNLRG YGMASPLGAA PSLTPPQLAT PNLQQFFPQA TRQSLLGPPP VGVPMNPSQF180
NLSGRNPQKQ ARTSSSTTPN RKDSSSQTPM VEDKSDPPFG SEEAEPKMD TPEDQDLPC240
FEDIAEKRT PAPEPEPCAA SELPAKRLRS SEEPTEKEPP GQLQVKAQPG AG 292

(2) INFORMATION ON SEQ ID NO. 357:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 169 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

PRRLPSVAVG MVRPAVSYVA GGIANWSSPC NCKSKALCR MEPLRREAEI VPWRFSGCC 60
GCCGGPPLTP WQRACGGDCW SSCWSCSNCC CCNCCWSCC CCNCWSCCC CWSCCCCCWL120
NMVARLPARP QRSSRFHGAW GPAAPTFRPG GSGPRAPGLP AATPGPVGS 169

(2) INFORMATION ON SEQ ID NO. 358:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 158 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

ISKTKKYCGS PSSRIRLEGG HLEMRKARGG DHVPVSHEQP RGGEDAAAE PRQRPEPELG 60
LKRAVPGGQR PDNAKPNRDL KLQAGSOLRR RRDGLGEAE GQLAPRDGVI IGLNPLPDVQ120
VNDLRGALDA QLRQAAGGAL QVVHSRQLRQ APGPPEES 158

(2) INFORMATION ON SEQ ID NO. 359:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 119 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

QSLRTLNLKN KKVWLISLEP NSARGRSPGD EKGPGRGGPCA CVPRAAERRG GRCCPGAQAE 60
ARARAGAQTG CPGGPEAGQC QAQPGPETAG WLRPEETAG PWFPSCRGSAG PEGWGHHP 119

(2) INFORMATION ON SEQ ID NO. 360:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 187 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

PPEFGWDAAE TDLLLAEEGS GWRGPHGQV LGLLWRPRL SKLPAVDHLQ SSFSLAELG 60
 IQGATEVVHL DIRQGVKAND DIPRGQLTL CMRAKVPPSP PEVGASLQFQ VPVGLGIVRP120
 LAPRDSSEF QLWLWPLFGL LGSSVLPASR LLVGHRHMPV PAGLSHLQVT ALEFNSARGR180
 STVLFCE 187

(2) INFORMATION ON SEQ ID NO. 361:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

STILGKSRI EFFSRCPTRV GQGFQSRLLN SHRIQTPGKI ALRSQLLSSL YGSRKNSTKM60
 TGHFMSVMEM KPHLLEKPLN QNYLFS 86

(2) INFORMATION ON SEQ ID NO. 362:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

ITKAIVFSFV FSSGYTVEVR ESLILLFGAI IKAMQPKIK HFGSSQDDMS GDRSCGSHSN60
 NLMGPKEKTG VNVLSFYMQ ELC 83

(2) INFORMATION ON SEQ ID NO. 363:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 117 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

YKNDRSSYER HANETPSSGE ALESELSFFL MSSDAASFLI FLKTVCF CGM YICTPNYLAL 60
 GNHSTTQRQL NKEKENFKYQ VLSNISQTS D FIKGLPANKV HPKYTG EKAR LLQGPRV 117

(2) INFORMATION ON SEQ ID NO. 364:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 83 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

SCRCFYCPMD MPLTRFWTP NSPRMTRRHS HVICIFYQL QIVALLRLFP VQQEMERKHF60
 SFLHTTPLDN WKYFWVITIL GYF 83

(2) INFORMATION ON SEQ ID NO. 365:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

QYGPSRVEVE MSYRIANTLG SFLPRLAQSR QQQQNVEDAM KEMQKPLARY IDDEDLDRML 60
 REQEREGDPM ANFIKKNKAK ENKNKKVRPR YSGPAPPNNR FNIWPGYRWD GVDRSNGFEQ120
 KRFAFLASKK AVEELAYKWS VEDM 144

(2) INFORMATION ON SEQ ID NO. 366:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

KPTKHRCCQH PKKYRYLNPV IRSRIFFCGQ NWHSTSCWSV WAPIISTDNC YHWISRLCP 60
 LPQPSHPHSL RKVTYPQHSI CRQVPELPSC WQAWQSASVQ IHWICPLRPS DIQARY 116

(2) INFORMATION ON SEQ ID NO. 367:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 160 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

SSENFPNTAA VNTPRSTGTS IQTSGLEYSS VVKGTGIQVVA GLCGLQLLAQ TTVTTGYLAA 60
YAHYHSPATP TASGKLHILN TPFVGKFLHC LLAGKPGKAL LFKSIGSVHS VPAISRDPDIK120
SVGRRCWTV ARSHFFILVL LGLILLDEVG HRVPLSFLFS 160

(2) INFORMATION ON SEQ ID NO. 368:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 227 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

WESMNRWYVK PLETSSSKVK AKTIVMIPDS QKLLRCELES LKSQLQAQTK AFEFLNHSVT 60
MLEKESCLQG IKIQGLEEV L SPTGRQGEKE EHKWGMQGR QELYGALTQG LQGLEKTLRD120
SEEMQRARTT RCLQLLAQEI RDSKKFLWEE LELVREEVTF IYQKLQAQED EISENLVNIQ180
KMQKTQVKCR KILTKMKQQG HETAACPETE EIPQEPVAAG RMTSRRN 227

(2) INFORMATION ON SEQ ID NO. 369:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 155 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

FIFSLEGSSG RAVPAAQAGG KGGALLKGG WERSWSESES ESQEGSGGLR HWCPLWPLRL 60
 EALGQAPEHK VRLSMEFCST CTADHISLSS FWRSSFQQPL APAVSLQSPD RRLSHDPAAS120
 SWSGFCGISP AFSAFSECSF SSLRSHPPAL GASDR 155

(2) INFORMATION ON SEQ ID NO. 370:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 114 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

DLILLRLELL IDEGHLLPHQ FQLLPQELLA VPDLLGQQLQ AASGAGPLHL LTVTQGLLQF 60
 LKALGQGPIQ LLPALLHAPL VLLLLSLAAC GAQHLFKLIN LDLLQAALLL QHGH 114

(2) INFORMATION ON SEQ ID NO. 371:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 201 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

TASTLRAVFP RPASESPFLR ARSDAEDLTA AMSSNECFKC GRSGHWAREC PTGGGRGRGM 60
 RSRGRGFQFV SSSLFDICYR CGESGHLAKD CDLQEDACYN CGRGGHIAKD CKEPKREREQ120
 CCYNCGKPGH LARCDHADE QKCYSGGEFG HIQKDC TKVK CYRCGETGHV AINCSKTSEV180
 NCYRCGESGH LARECTIEAT A 201

(2) INFORMATION ON SEQ ID NO. 372:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 189 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

LATAVTVDFT CLAAVDGYMT SFTTPIALHF GAVFLNVSEF STRIAFLLIC MVAVTSQMAW 60
 FATVVAALLS LSLGLLAVLG NVATSTAVIA GILLKITILG KMTRLTTAIT NIWKRRGNKL120
 ETSATASHST TTAATSTRTP GPVARSTLE ALIAARGCSQ IFRVGAGPQR RRLGRRPGED180
 GSQGRGCLF 189

(2) INFORMATION ON SEQ ID NO. 373:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 316 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

GGDPVVSSTY RSVGCSEQQK PASSDVVLPA TMSYTGFEVQG SETTLQSTYS DTSAQPTCDY 60
 GYGTWNSGTN RGYEGYGYGY GYGQDNTNY GYGMATSHSW EMPSSDTNAN TSASGSASAD120
 SVLSRINQRL DMVPHLETDM MQGGVYGS GG ERYDSYESCD SRAVLSEDL YRSGDYSEL180
 DPEMEMAYEG QYDAYRDQFR MRGNDFGPR AQGWARDARS GRPMAAGYGR MWEDPMGARG240
 QCMSGASRLA LPLLPEHPR VRHVEGACEV GAPSRASRF GFRVWQWHEA DEGLGRRPGF300
 QPICEPRRRR ESRAAF 316

(2) INFORMATION ON SEQ ID NO. 374:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 200 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

```

IPAAALLTGS I RMPPCFLFFF LVRKSAVVVF FVVRPHLLHA IAKPENQNGK PFGKAPQFRM 60
PLEHAVLGDD VLGEEGGQAE RHQTCTGPGP PWGLPTCAHS LRPLAGRS GH PGPSPVPWDR120
RCRCHACGTG RGRHRIGPHR PFPSQGQARC SHSLTGTGRA HSGRPSSRRT HKSHTFLHLS180
RTRLASCLS PNAAPYLSAG                                     200

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(2) INFORMATION ON SEQ ID NO. 375:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 218 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

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STSHDCVPQA DAAAYSRTAD GETEARGGRG GADLPASPS P RPLAPWPV RSTRGARRRR 60
TARGQAGSSS AMAAQRLGKR VLSKLQSPSR ARGPGGSPGG LQKRHARVTV KYDRRELQRR120
LDVERKWIDGR LEELYRGMEA DMPDEINIDE LLELESEER SRKIQGLLS CGKPVDFIQ180
ELLAKLQGLH RQPGLRQPSF SHDGLSLFLQ DRARTARF                                     218

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(2) INFORMATION ON SEQ ID NO. 376:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

NQLKLLKQQAG SFSQEGCKGE NILSFLQGN HCPGVFPASGR HNLSKVQGM LARKGGILDCC 60
 LLSEPSPTPQ PASWCLFSSK LSLPNLSSSE GKRESVPGFS RVGERTGKGT DI 112

(2) INFORMATION ON SEQ ID NO. 377:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

VRPEHSLMVL SLDTPTSYLQ FSRRRASGTL GCKPNLGSMT ALNPNSQRRS ECIFHHAAAG60
 CWRPFCVFSQ PSEITSFLVA VTNSWTTMK LIYFFI 96

(2) INFORMATION ON SEQ ID NO. 378:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

SNRLVASPKK DARVKTFFPS FCREIIALVC QPVVGTTQK FKGCWLEKEV FWIAASSQNP 60
 LLPHSLLPPGV FFPNSLYLT SLHQKASGNL FRVSVWEKXG QAKAQIFRRE SSYFWPLHVP120
 YSGIVGPDOW HSDSQLNFW E NIRGS 145

(2) INFORMATION ON SEQ ID NO. 379:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 429 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

RQFEITSISV DVWHILEFDY SRLPKQSIGQ FHEGDAYVVK WKFMVSTAVG SRQKGEHSVR 60
 AAGKEKCVYF FWQGRHSTVS EKGTSAIMTV ELDEERGAQV QVLQCKEPPC FLQCFQGGMV120
 VHSGRREEEE ENVQSEWRLY CVRGEVPVEG NLEEVACHCS SLRSRTSMVV LNVNKALIYL180
 WHGCKAQAH T KEVGRTAANK IKEQCPL EAG LHSSSKVTIH ECDEGSEPLG FWDALGRRDR240
 KAYDCMLQDP GSFNFAPRLF ILSSSSGDFA ATEFVYPARA PSVVSSMPFL QEDLYSAPQP300
 ALFLVDNHHE VYLWQGWPI ENKITGSARI RWASDRKSAM ETVLQYCKGK NLKKPAPKSY360
 LIHAGLEPLT FTMNMFSEWH REDIAEITEM DTEVSNQITL VEDVLAKLCK TIYPLADLLA420
 RPLFEGSIL 429

(2) INFORMATION ON SEQ ID NO. 380:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 169 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

DVFHEGDLIG NFRVHLCOLS DVLSVLPAGK HIGECQGLQT SVDKVRLGGW FLEIFSFAVL 60
 EHS LHRTLEV GGPADAGGTS DLVLDGPPAL PEVHLVVIWN KEKCWLGRAV QIFLQEGHGT120
 DHRGSGSRVH KLCGCKIPRG AAEDQAGRE VKTSRILKHA IVGFVPS 169

(2) INFORMATION ON SEQ ID NO. 381:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 234 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GIPSEWLGA FITLVYCDFA ATMQSCFQGT LFLDLVRS GP SDLLRVGLGF ASVPQVDEGL 60
 VDVKHHHGSS GPQAATVTGH FQIIPFHGHL STHAVQPPLT LHIFFLFPP PRVHHHPPE120
 TLQETGGLLS LENLDLGPFF LVQLHRHQRR RALLTHGGVF ALPEEVDALL FAGCPHRVLS180
 LLATSHCRAH HELPLDHIGI PLMELPDALF GEPAIVEFQD VPDHGNAGD LKLF 234

(2) INFORMATION ON SEQ ID NO. 382:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 81 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

RLFAPLRTSW AVVIFGARVA LCFYKIMTYV TCLHVCLLVE FLNSQLTNHR KYFSLSYGF60
 FTGLRGFSEY LWPQHTQFP S 81

(2) INFORMATION ON SEQ ID NO. 383:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

IVNRTTACTL FEVNLEWKAR DYTLEFKIDIC GAHTIYEIVP SKKEKKKIRR SNLEQHCLIK60
 A 61

(2) INFORMATION ON SEQ ID NO. 384:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

PPDFFFLFFR GYFYICVSP TNVYFKKSIV PGLPFQIHLK ESTCSPVYN LIEMRK 56

(2) INFORMATION ON SEQ ID NO. 385:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

LOSSHCCSCS TALFRTQTTA AAVPRMVIRV YIASSSGSTA IKKKQQDVLG FLEANKIGFE 60
EKDIAANEEN RKWMRENVPE NSRPATGYPL PPQIFNESQY RGDYDAFFEA RENNAVYAFLL20
GLTAPPGSKE AEVQAKQQA 139

(2) INFORMATION ON SEQ ID NO. 386:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 95 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

ETKHILLFLL NRCRARGRCN IYTDHHPGNS GCGCLGPEKG CGAAAAMAGI QLGAETAVGR60
EGWGKVEGEL ARAPFFPLAA STELSKRCSS SPKPR 95

(2) INFORMATION ON SEQ ID NO. 387:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 96 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

FCIRFECLHV KTQLIYYFNI KPISFEAKLI LLFYKSNGDS FFRMLKAQCL RFMLAALLAL60
LLPLNQVGLS SLRRHTLHYF LWLQRRHSP RDTGFH 96

(2) INFORMATION ON SEQ ID NO. 388:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 221 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

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FIMLNIIILIK FSSFSIRCAI LSSVCLNEAI TFAFLQVFL WNMDKYTMIR KLEGHHHDVV 60
ACDFSPDGAL LATASYDTRV YIWDPHNGDI LMEFGHLFPP PTPIFAGGAN DRWVRSVSFS120
HDGLHVASLA DDKMVRFWRI DEDYPVQVAP LSNGLCCAFS TDGSVLAAGT HDGSVYFWAT180
PRQVPSLQHL CRMSIRRVMP TQEVQELPIP SKLLEFLSYR I 221
  
```

(2) INFORMATION ON SEQ ID NO. 389:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

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KGGATCPESP QDRKRGNLD MEKLYSENEG MASNQGMEN EEQPQDERKP EVTCTLEDKK 60
LENEGKTENK GKTGDEMLK DKGKPESEGE AKEGKSERE ESEMEEVERE GTRGRGSG 118
  
```

(2) INFORMATION ON SEQ ID NO. 390:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

RFPYLGFPPLS RPPPSLTLPPL SLTFLLPLP HSLAFLYPLT FPHLLFCPCF LSFFRFLTSC 60
 LPEYKLLAF SRLVAVLHFP SFLGLKPFLH FHCVRVPCRD FPSFSCPAGI LDRLLLLFSF120
 AERWEQQTRR PGRSWTKN 138

(2) INFORMATION ON SEQ ID NO. 391:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3218 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GCGACCACGA GCTGGTGCAT CCATCAGTAC CCTTGCCGGA CTTTCCCTTA AAGAAGGAGA 60
 GGATCAGAAA GAGATAAAGA TTGAGCCAGC TCAGGCTGTG GATGAAGTGG AACCTCTACC 120
 TGAAGACTAT TATACAAGAG CAGTAAATTT AACAGAGGTA ACAACCTCTC AGCAGCGTCT 180
 GTTACAGCCT GACTTCCAGC CAGTCTGTGC TTCACAGCTC TATCCTCGCC ACAAACTCT 240
 TCTGATCAAA CGGTCCCTGC GCTGCCGTAA ATGTGAACAT AATTGAGCA AGCCAGAATT 300
 TAACCCACAG TCAATCAATT TCAAAATCCA GCTGGTGCCT GTCAATTATA TTCGAGAAGT 360
 GAGAATCATG TCAATTCCCA ACCTTGCCTA CATGAAGGAG AGCCAGGTCC TCCTGACTCT 420
 TACAAATCCA GTTGAGAACC TCACCCATGT GACTCTCTTC GAGTGTGAGG AGGGGGAGCC 480
 TGATGATATC AACAGCTGCT CTAAGTGGT GGTGCCCTCC AAAGAGCTCG TTGTAGTCTG 540
 CAAGGATGCA GCAGCAGAGT ACGATGAGTT GGCAGAACCT CAAGACTTTC AGGACGATCC 600
 TGACATTATA GCCTTCAGAA AGGCCAACAA AGTGGGTATT TTCATCAAAG TTACACCACA 660
 GCGTGAGGAG GGTGAAGTGA CCGTGTGCTT CAAGATGAAG CATGATTTTA AAAACCTGGC 720
 AGCCCCCATT CGCCCCATTG AAGAAAGTGA CCAGGGAACA GAAGTCATCT GGCTCACCCA 780
 GCATGTGGAA CTTAGCTTGG GCCCACTTCT TCCTTAAAGG GTTCCACTGG AGGGCAGATC 840
 CCAAAGGACA GTATCACCGT AAACCTGCGT TAAAAATGTG AAGCTGCTGC TTCATTAGGC 900
 CTTGTTTATA ACGATGTACC CATGCACTAC GGAATTTCTA TGCTAAGAAA GTGGGAGCAT 960
 AGGCAAGGCA TTGGGAACAC AGGGTAGCTG CTGTCTCACC CTGTGTGACA1020
 CCAGTAAGTC TGTGTTCTCC TCACCTGAACC CTGACGTTG AGTAACAGCA GCATAATTC1080
 ATCCTAGGAA AGGGGATGAG TGTCTCTTGG AATGGCACTG TATTTACACAT CTGAGAAACT1140
 CTGTACTGTC TCTTGATCTG ATCTCACTAA GGATCACAAT GTCACAGATG AAACTTAAAT1200
 GATAACCCAA AGGTAGACCT GCTGTTAATG ATCCAGCATT GGTCAACAATG TACCAACTGC1260
 TTTCTGCATT CGGTTAATA TCACTAACA GTCTAAACCA TATCCCTTCA TTGCCATPAT1320
 GGCTGCCATT TTGCCATAGA TTTCCATATA ACTGAAACAC TGAATTGTCA CTTTATCTTT1380
 AGTATCATGA TGATTGGAAA AACCTGTGAA GTTGTTAAGG CACTCTCATT TGGCCTTTT1440
 TTCTAAGTGA ATACAGGACA CGTATTAGTT GTTCTTAANN NNNNNNNNNN NNNNNNNNN1500
 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN GGTAGCAGAT1560
 TCCATTGCTT TTCAATATTG CCACAATACC CAGGGATTAA TGCTGCCACA GGGGGGCAAT1620
 CTTTATTGTT CTTACTTCCT ACCCCTTCCC TGTCTGCTCT CTTTAACTCA GTTAAGTTGT1680
 TCTGTTTGGG ACCTGGA AAAA GAACCCAAAG AAAACCTGAG TGGACAGGTT CATTTCTGAI1740
 ATGCAGAAA CAATTTAAAG GCTAGATTTT TAGAATATTC TCAACTAGCA TTCTTCCAT1800
 TGATTGGAAG GGGAAATTA TATTATAAT CTCTGATTC CAAAACCTGGA TATTAAAGAC1860
 TTTCCCTCTT ACTAAGTTTA AGACTTTTGT CATGTGGTGA GTCAAAATAAG ACCATTTGAI1920
 TTGTAAACCA TAAATAGTT CAGCAAGTAG CCCACAGTTT TGGCCTTAACA GCAGACTTGC1980
 TGTGTTCACT TGGTATCCTG GAGTTGGGTT GCTAACCTTA ATTTCTATGA TGTGTTCTAA2040
 AATGAAACTT GATAAAGTAG ACCACGAGCT GCACCGTGT TTCTGTAAAA GTATTGTTAG2100
 TAAGTGCCCA AGAGACTTGA GGAATAACA GATTTTTTGT TTACCTTGGT CTGTGTTTAA2160
 GTCTTAAAAA ATTAAGATA ACATTATAAT GTAGAATACA TTAGGACAT AGTCCTTGTA2220
 AGCTTCCCTT GAAATGTTT TAAATATTTA GGAAGCTTTT AAAAGACAT AAATTTGACT2280
 CTAAAGACA CTAATATGTA CTAATTGTAC AAAGGTCAAG CCAATTTTAT GAACAGTCC2340
 TACAGAGTAA TATATGTGAT GCAGTGTAA GAGGAAATA CTATCTCTA ACATTATGGT2400
 AATAACATTT AGCCTCTTAG GAGTTGGAGC AGGGGGATGG GTAATTACAG ATTTGCAGAC2460
 TATGAARAGA GTTTCATTTT TTTGTGACCC CACAGAGTCT CAAATTTTTC TTTACCTACC2520
 TGCTAGAGCC TACTGTGAAA TCACTGCTCC ATATTGGCCA GTGGAGGAAA TGGGATAGA2580
 TAGAGAATA GCTTCATATG GTTTACAGCT TTGCATAGAC TACACACATG TACTGCGTT2640
 ATGGCAGGTA GCTGGTATTT ATCCCAAGAG TAATAATGTT GAAGTATGGG TCTCATCAT2700
 CCCATACACA GAAACACAAA ACACCTTTGAT CATAAACTTT TTCTTTCAGA AGCCAAACTA2760
 ACTTGCAGAA TAATAGAGGC ACTGGTTTAA TGTGTTCTCA AGATAGGTTT TAGTGTAAAG2820
 TAGTTATCTG TGTGTTCTGA GAAATGATTC AATACCTGCA CCGTGTGAAT TAGGAATTGT2880
 ATTTGTTGGC TTTTATATAT TAGATGAGGT GCAAAATTTT TAATGCTAGT CAGTATGCAC2940
 CACCCACAGGA AAGTTAGATC CCATTAGCAC TTGAAACTAC AGCTTTGGAA ATTTAGGCTA3000
 AGTTAATTTG GATTTGTTAC TACTGACCTT TCTTTTGTGT TGAAGTGGCT3060
 ATCAGCATAA TGAGCTAAGT GTCATGCATA TTTGTGAAGA AACACCCCTT TTGTTCCCTT3120
 TTGGGACAGA GAGGTACTCC TTGATCTTTA TGAATGACAG GTTACTGTGT TGCCTTTATG3180
 CTTAACTTAA TGTAGTGAAG TAAAGCAGAC AAGGCTTG 3218

GCGACCACGA GCTGGTGCAT CCATCAGTAC CCTTGCCGGA CTTTCCCTTA AAGAAGGAGA 60

(2) INFORMATION ON SEQ ID NO. 392:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 750 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

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GTGAGGGACA GATGGACAGA ATGCAGAGGT ACATAGATGA GCTGAGGCTG ATCCAGCTCC 60
CCTGAAATTC AGAGTGTTAA CTTGTAGAC  CCTGCACAAT CTCTTGGTGC TATCTAGCCAL20
TTACCCCAT  TTTTTTTTA  AAGGCCATCT GAAATTCAT TTCTCATGCT GGGAGACATT180
TTGGATATGA TGCAGGAAAT CTCCTCCTGG AGTCAAAAGT TCCCAAGAGG TCCTGTATTT240
TTAAGAAATG GAATTTATTT AAATAATATT TAAGCTTGTG CCCATGTTGG CCGGGCAACT300
TTTTTCATG GTGCTTATTA GAAGAAGTTT TTTCACTTGT TCATTTTAAG AAAATAAAAC360
TGGAAATGA  ATATGGGTGG CATGATTGTA CCTTTTAGT  TCTCTTATTT TTCTACTCCT420
CTGTCCTCTC ATAACATATG CATACTATTA GATGCTGGTC CACTGAATGC TGAGATGATC480
TGTTTTTTTG GGTTTTTTTT TTTTAAAGAA TATTTTCACT GGTTTTCTGT GACTCTCTAA540
ACACTTCATC GAAACTAGGA AGACTGAATT ATGAGGGAAA CTATTGGGGA TTAGTGGCCA600
GAAACGATGA AATCTTATAG ATCTTTTAC AGTTTCTCTG TTAGGGGGA GCCTAGGACT660
GATATCCAG  TTTCTTCCAT ATCCAAGCTT CATTGGGGGA CCCCATTG  GCTTTAACAG720
GTGACCCGGC CCTCTTACC  GGGCTTCCAG                                750

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(2) INFORMATION ON SEQ ID NO. 393:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CACGAGGAGG CCGGGAGTGG AACCCCTCT TTTGAGAAGG TTGCCTGACT CAGAGACACA 60
GAAACGGGTC CAGGGATGGG GAGAGATGTG GAGTGAGGGA AGGTTTGCAT TTGAGAAAGG120
AAGTTTCGAGA ACACACTGGG ACATTGTAAC ACATTTGAAC CATCTTCTGA TAGAAAGGTG180
TTGGCCTCCT AATAATGGGA GGTGAGGGCC AGGTCCCTCG GCATAGGGAG AGGGTCCGGA240
GAATGCTGCA GACCCCTGCC CACTGCCAC GGTCTCCGCT CCCTGCACCT GCCTCTGATG300
GTGCAGCTCT GATTCCGTGT CTCTCCTCAT TGCAGATTTA TGAAGGTGCC TACCATGTTG360
TCCACAAGGA GCTTCCTGAA GTCACCAACT CCGTCTTCCA TGAATAAAC ATGGGGTCT420
CTCAAAGGAC AGCCACGGCA GGAACCTGGT CCCCACCTG AATGCATTGG CCGGTGCCCG480
GCTCATGGTC TGGGGGATGC AGGCAGGGGA AGGGCAGAGA TGGCTTCTCA GATATGGCTT540

GCAAAA

546

(2) INFORMATION ON SEQ ID NO. 394:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2453 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

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CCTGACGGGA CCAAGCGGCG GGGAGTCTGC GGTGCTGTCC TCGGCTGTGG ACCGGGCGGC 60
ACGACGGCGT GCAGGGTAAAC ATGGCGGATG CGGAAGTAAT TATTTTGCCA AAGAAACATA 120
AGAAGAAAAA GGAGCGGAAG TCATTGGCAG AAGAAGATGT AGCCGAAATA CAACACGGTG 180
AAGAATTTTT TATCAAAACCT GAATCCAAAG TTGCTAAGTT GGACACGCTCT CAGTGGCCCC 240
TTTTGTCTAAA GAATTTTGAT AAGCTGAATG TAAGGACAAC ACACATATACA CCTCTTGAT 300
TGTGTTCAAA TCCTCTGAAG AGAGAGATTG GGGACTATAT CAGGACAGGT TTCAATTAATC 360
TTGACAAGCC CTCTAACCCT TCTCCCATG AGGTGGTAGC CTGGATTGGA CGGATACCTC 420
GGGTGGAGAA GACAGGGCAC AGTGTACTC TGGATCCCAA GGTGACTGGT TGTTTAATCG 480
TGTGCATAGA ACGAGCCACT CGCTTGTTGA AGTCACAACA GAGTGCAGGC AAGAGTATG 540
TGGGGATTGT CCGGCTGCAC AATGCTATTG AAGGGGGGAC CCAGCTTTCT AGGGCCCTAG 600
AAACTCTGAC AGGTGCCTTA TTCCAGCGAC CCCCACTTAT TGCTGCAGTA AAGAGGCAGC 660
TCCGAGTGAG GACCATCTAC GAGAGCAAAA TGATTGAATA CGATCCTGAA AGAAGATTAG 720
GAATCTTTTG GGTGAGTTGT GAGGCTGGCA CCTACATTCT GACATTATGT GTGCACAGTG 780
ATCAGTCACG CGCACGAGGT ACGTCAGATG CAGGAGCTTC GGAGGGTTCT TTCTGGAGTC 840
ATGAGTGAAA AGGACCACAT GGTGACATG CATGATGTGC TTGATGCTCA GTGGCTGTAT 900
GATAACCACA AGGATGAGAG TTACTGCGG CGAGTTGTTT ACCCTTTGGA AARAGCTGTT 960
ACATCTCATA AACGCTGGT TATGAAAGAC AGTGCAGTAA ATGCCATCTG CTATGGGGCC1020
AAGATTATGC TTCCAGGTGT TCTTCGATAT GAGGACGGCA TTGAGGTCAA TCAGGAGATT1080
GTGGTTATCA CCACCAAAAG AGAAGCAATC TGCATGGCTA TTGCATTAAAT GACCACAGCG1140
GTCATCTCTA CCTGCGACCA TGGTATAGTA GCCAAGATCA AGAGAGTGAT CATGGAGAGA1200
GACACTTACC CTCGGAAGTG GGGTTTAGGT CCAAAGGCAA GTCAGAAGAA GCTGATGATC1260
AAGCAGGGCC TTCTGGACAA GCATGGGAAG CCCACAGACA GCACACCTGC CACCTGGAAG1320
CAGGAGTAGT TTGACTACAG TGAGTCTGCC AAAAAAGAGG TGGTTGCTGA AGTGGTAAAA1380
GCCCCGCGAG TAGTTGCCCA AGCAGCAAAA ACTGCGAAGG GAAGCGAGGA GAGTGAGAGT1440
GAAAGTGACG AGACTCCTCC AGCAGCTCCT CAGTTGATCA AGAAGGAAAA GAAGAAGAGT1500
AAGAAGGACA AGAAGGCCAA AGCTGGTCTG GAGAGCGGGG CCGAGCCTGG AGATGGGGAC1560
AGTGATACCA CCAAGAAGAA GAAGAAGAG AAGAAGGCAA AAGAGGTAGA ATTGGTTTCT1620
GAGTAGTGAA GGCCACTTGA AGCTGGAGGA GAAACTAAAG CCTTTATTGAG AAAACATGTT1680
ATAGATCCTT TTGTTGCTGA GAGAGTGGAA CATAGTCTCT AGACAGGGTG AAGAGTTCTG1740
GCACATTTTA GCTGCTACTT TGAGACCTCG GTGATGTTAC CTGGTGTTGG CATCCCATCT1800
TGCTCTGTTT TAAGGATATA GGTGGTGAAA GATGAAAGAG GCAGAGTTTA TCCCAATGAC1860
TTCTCTGTTT GAGTTGGGAA GCCTCACCTT CAGACCCAGT AACTGTCCGC AGCTGTCTGC1920

TAGTGGTTGT CTTAACAICG TAGTCCTAGT TTGCATTTT TAAATCCCCT CTGTTTAAAA1980
GGTTTGTAAA ACAAAAAACA AAAACTAAGT CTGCTCAGTG AAATGCTGTA GAACCCCTAAA2040
TAAGTGGTAG AAGAGTGTC ACGAATTTTG TCTCTGAATT CAGTATAACT GAGTTTGTCT2100
CATGCTGGTG TCTGGGTTAT AGGCCTGATG GGCTGGTAG TTTTCCATCT TGGTTCTGGCC2160
TAGAGGTACG TCCTTTGCAC TTCTCAAAAG CTTGTGTACA GTGCTCACCT AAATCCATCT2220
GACTACTTGT TCTGTGCCCC TCTTGTTTTA GGCTCGTTT ACTTTTAAAA AATGAAATTG2280
TTCATTGCTG GGAGAAGAAT GTTGTAATTT TTACTTATTA AAGTCAACTT GTTAAGTTT2340
TTATGTATTC CTGTTGGGTT TTCTTGTGTA TCTCATGCTA GCAGAGCAAA AATTGTAAAA2400
TATTTTGATT AAAAACTAGG GGACCTTTAT GTCTATTGTT AAAAAAATAA AAT 2453

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(2) INFORMATION ON SEQ ID NO. 395:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2706 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

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GGGAGGAAGG AGACTACACC TGCTTTGCTG AAAATCAGGT CGGGAAGGAC GAGATGAGAG 60
TCAGAGTCAA GGTGGTGACA GCGCCCCGCA CCATCCGGAA CAAGACTTAC TTGGCGGTTC 120
AGGTGCCCTA TGGAGACGTG GTCACGTAG CCGTGAGGC CAAGAGAGAA CCCATGCCCA 180
AGGTGACTTG GTTGTCCTCA ACCAACAAAG TGATCCCCAC CTCCTCTGAG AAGTATCAGA 240
TATACCAAGA TGGCACTCTC CTTATTCAGA AAGCCACGCG TTCTGACAGC GGCAACTACA 300
CCTGCTTGGT CAGGAACAGC GCGGGAGAGG ATAGGAAGAC GGTGTGGATT CACGTCAACG 360
TCCAGCCACC CAGATCAACG GGTAACCCCA ACCCCATCAC CACCGTGCAG GAGATAGCAG 420
CGGGGGGCGC TCGGAAACTG ATTGAGTGCA AAGCTGAAGG CATCCCCACC CCGAGGGTGT 480
TATGGGCTTT TCCCGAGGGT GTGGTTCTGC CAGCTCCATA CTATGGAAC CCGATCACTG 540
TCCATGGCAA CGGTTCCCTG GACATCAGGA GTTTGAGGAA GAGCGACTCC GTCCAGCTGG 600
TATGCATGGC ACGCAACGAG GGAGGGGAGG CCAGGTTGAT CCTGCAGTCC ACTGTCTCTG 660
AGCCCATGGA GAAACCCATC TTCCACGACC CGATCAGCGA GAAGATCAGC GCCATGGCGG 720
GGCCACAACA TTCAGCCTCA ACTGCTCTGC CGCGGGGACC CCGACACCCA GCCTGGTGTG 780
GGTCCTTCCC AATGGCACCG ATCTGCAGAG TGGACAGCAG CTGCGACGCT TCTACACCAA 840
GGCTGACGGC ATGCTACACA TTAGCGGTCT CTCCTCGGTG GACGCTGGGG CTTACCGCTG 900
CGTGCCCGCG AATGCGCGTG GCCACAGGGA GAGGCTGGTC TCCCTGAAGG TGGGACTGAA 960
GCCAGAAGCA AACAAAGCAGT ATCATAACTT GCTCAGCATC ATCAATGGTG AGACCCCTGAA1020
GCTCCCTTGC ACCCCTCCCG GGGCTGGGCA GGGACGTTTC TCCTGGACGC TCCCAATGG1080
CATGCATCTG GAGGGCCCCC AAACCCCTGG ACGCGTTTCT CTTCTGGACA ATGGCACCC1140
CAGCGTTCTG GAGGCTCTCG TGTTTGACAG GGGTACCTAT GTATGAGGGA TGGAGACGGA1200
GTACGGCCCT TCGGTACACA GCATCCCCGT GATTGTGATC GCCTATCCTC CCCGGATCAC1260
CAGCGAGCCC ACCCCGGTCA TCTACACCCG GCCCGGGAAC ACCGTGAAAC TGAACCTGCAT1320
GGCTATGGGG ATTCCCAAAG CTGACATCAC GTGGGAGTTA CCGGATAAGT CGCATCTGAA1380
GCCAGGGGTT CAGGCTCTGC TGTATGGAAA CAGATTTCCT CACCCCGAGG GATCACTGAC1440

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CATCCAGCAT GCCACACAGA GAGATGCCGG CTTCTACAAG TGCATGGCAA AAAACATTCT1500
CGGCAGTGAC TCGAAAACAA CTTACATCCA CGTCTTCTGA AATGTGGATT CCAGAATGAT1560
TGCTTAGGAA CTGACAACAA AGCGGGGTTT TTAAGGGAAG CCAGGTTGGG GAATAGGAGC1620
TCTTAAATTA TGTGTGCACAG TGCATGGTGG CCTCTGGTGG GTTTCAGTT GAGGTTGATC1680
TTGATCTACA ATTGTTGGGA AAAGGAAGCA ATGCAGACAC GAGAAGGAGG GCTCAGCCTT1740
GCTGAGACAC TTTCTTTTGT GTTTACATCA TGCCAGGGGC TTCATTCAGG GTGCTGTGTC1800
TCTGACTGCA ATTCTTTCTT TTTTGCAAAAT GCCACTCGAC TGCCCTTCATA AGCGTCCATA1860
GGATATCTGA GGAACATTCA TCGAAAATTA GCCATAGACA TGAACAACAC CTCCTACCC1920
CATTGAAGAC GCATCACCTA GTTAACCTGC TGCAGTTTTT ACATGATAGA CTTTGTTCCT1980
GATTGACAAG TCATCTTTCA GTTATCTCTC TGTCACCTCA AAACCTCCAGC TTGCCAATAA2040
GGATTTAGAA CCAGAGTGAC TGATATATAT ATATATTTTA ATTCTAGATT ACATACATAC2100
AGCTACCAT TATATGAAA AAAGAAAAAC ATTTCTTCTT GGAACCTACT TTTTATATAA2160
TGTTTTATAT ATATTTTTTT TCCTTTCAAA TCAGAGGATG AGACTAGAAG GAGAAATACT2220
TTCTGTCTTA TTAATAATTAA TAAATTATTG GTCTTTACAA GACTTGGATA CATTACAGCA2280
GACATGAAAA TATAATTTTA AAAAATTTCT CTCCAACCTC CTTCAAATTC AGTCACCACT2340
TTCTGTCTTA TTAATAATTAA TAAATTATTG GTCTTTACAA GACTTGGATA CATTACAGCA2280
TATGCAAGT TTTTGTGAA AGCTGTGCTC AGAGGAGGTG AGAGGAGAGG AAGGAGAAAA2460
GTTATATTAC CTTCTCCAGG AACCTTCCAG TGGGGAAGTG TGCATATTA GATTTCCTTG2400
CTGCATCAT ACTTTACAGA ATTGAATCTA GAGTCTTCCC CGAAAAGCCC AGAAACTTCT2520
CTGCAGTATC TGGCTTGTCC ATCTGTGCTA AGTGTGCTGC TCTTCCCTCA GCCATGAGTC2580
AGTTTGTGCC CATGAATAAT ACAAGACCTG TTATTTCCAT GACTGCTTTA CTGTATTTT2640
AAGGTCAATA TACTGTACAT TTGATAATAA AATAATATTC TCCCAAAAAA AAAAAAAA2700
AAAAAA

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2706

(2) INFORMATION ON SEQ ID NO. 396:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2242 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

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CAGGCCGGGT CCGGCCGAAGT TAAACCCCTCG GAGCTGGCCT CGGACTGCTG GGGCGTTACC 60
CCTTCGGGCCA CCCCGCGTGA CCATGGCGAGT GTTTCATGAC GAGGTGGGAAA TCGAGGACTT 120
CCAATATGAC GAGGACTCGG AGACGTATTT CTATCCCTGC CCATGTGGAG ATAACCTTCTC 180
CATCACCAAG GAAGATTTCG AGAATGGGGA AGACGTGGCA ACGTGTCCTA GCTGCTCTCT 240
CATTATAAAA GTGATTTATG ACAAAGATCA GTTTGTGTGT GGAGAAAACAG TCCAGCCCCC 300
TTCAGCCAAC AAAGAATTAG TTAATGCTG AAGAAGCCTT CAGGAATCCA AATCCTGAAC 360
ATTTGGGAATG AGCCCGAGTA GAAATATGCA ATGCAAAGCT ACTGGCTTCA CAGAGACAAC 420
CATTTATGAT TTGCTGTTCT GTAAGAGTGT GGATTCCTTC TATCAACTTC TGATATCATC 480
TTCAGGAAGC AAGTCCATAA CATGACATAT CTGATTTTGT TGCTTAGAAC CTTAAATTGG 540
AAGCATTCCT AATTATGCAT CTTAAATTAA AAGAAGATAA TTTCAAAACA GTGCTTTCTT 600

TCCCTTGGTT TCATCATTTT CATATCTTAA ACCAAATTAC TTCGGTATCT GACACACGCA 660
TCATCTACCT CAGTCATTAG GATTTCTTAA TAAAAAGAG ATTGTATTTT TGACTTGGTT 720
ATTAAGATTA TTAAGATTAG CCCTTCCTTT GAAATATGAC ATCAGCTTTG CTGTTCTAAA 780
TTTAAATTA GTTGCTTCAT CAGTACCACA CTTCAGTTT CTATACCAG CCAGTCTCCT 840
CAGTTTTCCT ATTAGAATGG ACATGTTCTG TTCAGCGTGT CATTTCGTGA ATGCTTCATG 900
CAGAGAGTTT GGTTCATAGTA TTAAGAGAGAA AATACAGTGA GGTCAACAAT TCTCCAGAGC 960
TAAAGTTAG TGAACAAGAA AGAAAGTCCA AAATGAAGTG ATGAAAGAA GAGGACTTTT1020
CTTATATTC GCATATTCCT TGGAAGTCAG GACAAGATGA AAAGAAAAAC ATCCAAAAGA1080
AGTGAATTT GTGACAGAAT GAGAGGAGCA AAGCATACCA GTGTAGTAAG TGAATGTTT1140
GAATGACTTT GCCAGGTCAG AGCAAGTAAT ATTTCTGTAT CTGAGTTTTT GTTTGTGTTT1200
TGATAAGGCT AATGAAATTG CATTCAGGCT AGGGGTTAAC GTCAAAATTC CATGGCTGGT1260
AGCTGTGCTT TTGGCATAAT ACAGTGTGTT GTCACTACTA CAAGGTAAAG CATCTACAGC1320
GGAGAATGAG CTTGAAATG AGAGACCTAT TGTGAATAAA TATGCCCCATG AGAGCATATT1380
TAATAAGCCT CTATAACATG CAGCCAAACC AGACATTCAC TCCTGCAGAG AAATGTTGCC1440
CTGGAGAAAA AGAGATATAT AAAGATAGGC TATCACCCCT CTTTGTCTGC AGTACTAAGC1500
ATAGCAAGAA ATTAGAATCA TTTACATTGG AAATTTGAAA ATTCCTCTTA TATACACAAC1560
TTTACTGTGT ATAAATAAAA AATATTTATT AATGCAGTGA TGTCCGTCAG GTTGTTTTAG1620
GAATGGCTTC TGCAATTAGA AAAATAGCTT GCTAGAATGT AAATGTTCTG CTACTGGTAA1680
ATGTACTGCA CACATTCATT GGACGTTAAA ACAAGTGAGT AGCCTTTTTT ACCTGGCAGC1740
AGCATGGCTG TGTGAGGCA CTAGGCTGAG ACAATAAATT ACCAAAAAAT ATAATGTACC1800
GAGCTGAAAA TGCTCAGTAC ATTATGTGGC ATATTCGGA TGTGATGAGA AATCTCATTG1860
CCATTTGGGA CACTGACATC CCAGAAGTAA TCCACAACCT CACTATGGTG GCATCAGCTG CAAAGCGAAA1980
TGCTCAGATG AACAGAGCAG AGTACTCACT CACTATGGTG GCAACATCTG TAGCTCTTTC2040
TGAATGCTAT GAGTTTCAAA CACGAACAGA CACNCTTGAT GTGGGTTTGC TAAGAACAATA2100
GAGAACAGG AAGAAAAGTT GCCAGGTTT AAAAATCCCA GGGAAAAAAG AAGCATAAAA2160
AGCATTAGCA GTCACTGACT GATGATAATG CTTGCAATAA TGGGGAATGG TTTGTTTTC2220
TAAACCCCAA AATTATTTC TT

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2242

(2) INFORMATION ON SEQ ID NO. 397:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1239 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

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TAGTCATCCT ACAACATGT TTCTGTTACT TCCTAATATT AAAATAGCCA TTTTGGATTC 60
CATATTTAAA GTGCTCATTT GAGTGAAATT CAAATTAGAA AGAAAATATAT TAAAATGCGC 120
CTAACAAGAAA CCTCTCTTTC AGAATCCCTA TTCCTTGAAT CTGGGGTTTG AACTGCTTAT 180
TAAAGGCAGG CCTAAACTAA TTTGTGAGAA ATGAAGAAGT TTTAGTATAT AATTCTTTTA 240
AAAAATATCA ATTACGGCTG GGTGCGGTGG CTCAGGCCTG TAATGCCAGC ACTTTGGGAG 300

GCCAAGGCGG GTGATCACCT GAGGTCAGGA GTTCAAGACC AGCCTGGCCA ACATGGCAAA 360
ACCCTGTCTC TACTAAAAAG TAAAAAAAT TAGCCGGGCA TGGTGGCTTG TGCTTGTAGT 420
CCCACTTCAG TCTAAGTAGC TGGGACTACA GGCACGTGCC ACNAGGCCCA GCTAATGTGG 480
GTGTTTTGTT AGAGATGAGG TAGGGCCATA TTGCCCAGGC TCGTCTTGAA CACCGGGGCT 540
CAAGGAATCT GCCCATCTTC GCTCCCAA GTTCTGAGAT AGCAGGTGTG AGTCANTCAT 600
GCCAGCCTC CTGTAAGTTT ACTAACAAAT GGGATAACTG AGGGAAGAGA AGTGACAATT 660
CCACTCAGTC TATTAGAGGT CTGGATATRA GGTAGNCCAC ACAATACTC TAACNTGAC 720
TTCTAACCAT TCTATCTTAT TGNATTGGA GGCTGCTTC TGNCCAGATT TTTTGTGCT 780
TGAGATGATA TTTTNCGAAC CTTCTTTTCA CTACCTTTCT TACCCTTAAT GTGNCCAAGC 840
TTGAAACAGG ATTTGATTTT CTGAGCNTAC TTGTTTCGCC TTCTGTGCGT CANCCAAGTA 900
ATCTGGTTCA TCTTTCGNTN CTCATTCATG TTATTTTCAA GTGAACAAG ACATTTTGGG 960
GGNTCAAGTC TCNITTGGGN NGTTTTGTT TTTATGTATA TAAAAATGGA TTTTNGTGT 1020
CCCTTTCCNA TGTNAAGTAN CCAACTTATA TGGAACTCA CAATCATAT GTAAAGAAG 1080
AATGAAANGC CTGGTGTTAT GTACTTCAAG ATGCCTCCCT GNATGTATAG AATCCTCTT 1140
TAAAAATAAA TAATTGNCAT TGTATATCAG TCTTCCCATC AATATTAATT ATTAATATT 1200
TTAGAATTTT TAAATACCAA CTATAAAAA AAAAAAAA 1239

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(2) INFORMATION ON SEQ ID NO. 398:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1663 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

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GAACCTGCTC TCTCTGCTTG TGGTCCCTTG ACGCAGAGAC CGTTCGCTCC CCCACAGCCG 60
TTTGACTGAA GGCTGCTCTG GAGACCTAGA GTAAAAACGGC TGATGGAAGT TGTGGGACCC 120
ACTTCCATT CTTCAGTCA TTAGAGGTGG AAGGGAGGGG TCTCCAAGTT TGGAGATTGA 180
GCAGATGAGG CTGCGGATGC CCCCTGCTTT GACTTCAGCC ATGGATGAGG AGTGGGATGG 240
CAGCAAGGTG GCTCCTGTGG CAGTGGAGTT GTTGGCAGAA ACAGTGGCCA GTTGATCGC 300
CTATAAGACA GGGTAAGGTC TGAAGAGCTG AGCCTGTAAT TCTGCTGTAA TAATGATAGT 360
GCTCAAGAAG TGCTTGAGT TGGTGTACAG TGCCATGGCC AGCAAGAATC CCAGATTCCA 420
GGTTTTATTA CAAATGTAA GTGTCACTT GCGGATTTTG TAGTACATGC ATGAGTTACC 480
TTTTTCTCT ATGCTGAGA ACTGTCAGAT TAAACAAGA TGSCAAAGAG ATCGTTAGAG 540
TGCACAACAA AATCACTATC CCATTAGACA CATCATCAA AGCTTATTTT TATTCTTGCA 600
CTGGAGAAGT CGTAAGTCAA CTGTTTCTTG ACCATGGCAG TGTTCTGGCT CCAATGGTGA 660
GTGATTCCAA ATAATGGTTC TGTTAACTT TTGGCAGAAA ATGCCAGCTC AGATATTTTG 720
AGATACTAAG GATTATCTTT GGACATGTAC TGCAGCTTCT TGTCTCTGTT TTGGATTACT 780
GGAATACCCA TGGGCCCTCT CAAGAGTGCT GGACTTCTAG GACATTAAAG TATTGTCAG 840
TACATTAAAC TTTTCAATCC CATTATGCAA TCTTGTTTGT AAATGTAAC TTTCAAAAT 900
ATGGTTAATA ACATTCACCC TGTTATTAC AACTTAAAG GAAGTTTCAAT GAATTTGTTT 960

TTATTTTTTA ACAAGATTGG TGAAGTGAAT ATCATGAACC ATGTTTTGAT ACCCTTTTTT1020
CACGTTGTGC CAACGGAATA GGGTGTTTGA TATTTCTTCA TATGTTAAGG AGATGCTTCA1080
AAATGTCAAT TGCTTTAAAC TTAATTTACC TCTCAAGAGA CCAAGGTAGA TTTACCTCAT1140
TGTTATATA ATGTTTAATA TTTGTCAGAG CATTCTCCAG GTTTGCAGT TTTTCTCAT1200
AAAGTATGGG TATTTATGTT CTCAGTTACT CAAATGTTAC TGTATTGTTT ATATTGTGAC1260
CCCAATAAC ATCGTCTGTA CTTTCTGTTT TCTGTATTGT ATTTGTGCAG GATTCTTTAG1320
GCTTTATCAG TGTAATCTCT GCCTTTTAAG ATATGTACAG AAAATGTCCA TATAAATTTCT1380
CATTGAAGTC GAATGATACT GAGAAGCCTG TAAAGAGGAG AAAAAACAT AAGCTGTGTT1440
TCCCATTAAG TTTTTTTAAA TTGTATATTG TATTGTAGT AATATTCCAA AAGATGTA1500
ATAGGAATA GAAGAGTGAT GCTTATGTTA AGTCCTAACA CTACAGTAGA AGAATGGAAG1560
CAGTGCAAT AAATTACATT TTTCCAAAA AAAAAAATA AAAAAAATA AAAAAAGT1620
ATACGTTGGA ATGAAAAAAA AAAAAAATA AAAAAAATA AAA 1663

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(2) INFORMATION ON SEQ ID NO. 399:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2889 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

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GATCAGGCCT GTGGTCCAGC TCACTGCCAT TGAGATTCTA GCTTGGGGCT TAAGAAATAT 60
GAAAAAATTC CAGATGGCTT CTATCACATC CCCCAGTCTT GTTGTGGAGT GTGGAGGAGA 120
AAGGGTGGAA TCGGTGGTGA TCAAAAACCT TAAGAAGACA CCCAACTTTC CAAGTTCTGT 180
TCTCTTCATG AAAGTGTTC TGCCCAAGGA GGAATTGTAC ATGCCCCAC TGGTGATCAA 240
GGTCATCGAC CACAGGCAGT TTGGGCGGAA GCCTGTGCTC GGCCAGTGCA CCATCGAGCG 300
CCTGGACCGC TTTCGCTGTG ACCCTTATGC AGGGAAGAG GACATCGTCC CACAGCTCAA 360
AGCCTCCCTG CTGCTCGCCC CACCATGCCG GGACATCGTT ATCGAAATGG AAGACACCAA 420
ACCATTACTG GCTTCTAAGC TGACAGAAAA GGAGGAAGAA ATCGTGGAAT GGTGGAGTAA 480
ATTGTATGCT TCCTCAGGGG AACATGAAAA ATGCGGACAG TATATTGAGA AAGGCTATTC 540
CAAGCTCAAG ATATATAAAT GTGAACTAGA AAATGTAGCA GAATTTGAGG GCCTGACAGA 600
CTTCTCAGAT ACGTTCAAGT TGTACCGAGG CAAAGTCGGAT GAAAATGAAG ATCCTTCTGT 660
GGTTGGAGAG TTTAAGGGCT CCTTTCGGAT CTACCCCTCTG CCGGATGACC CCACGCGTGC 720
AGCCCCCTCC AGACAGTTTC GGAATTACC TGACAGCGTC CCACAGGAAT GCACGGTTAG 780
GATTTACATT GTTCGAGGCT TAGAGTCCA GCCCAGGAC AACATGGCC TGTGTGACCC 840
TTACATAAAA ATAACACTGG GCAAAAAAGT CATTGAAGAC CGAGATCACT ACATTCCCAA 900
CACCTCAAC CCACTCTTTC GCAGGATGTA CGAACTGAGC TGCTACTTAC CTCAGAAAAA 960
AGACCTGAAA ATTTCTGTCT ATGATTATGA CACCTTTACC CGGGATGAAA AAGTAGGAGA 1020
AACAAATTAT GATCTGGAAG ACCGATTCCCT TTCCCGCTTT GGGTCCCACT GCGGCATACC 1080
AGAGGAGTAC TGTGTTTCTG GAGTCAATAC CTGGCGAGAT CAACTGAGAC CAACACAGCT 1140
GCTTCAAAAT GTCGCCAGAT TCAAAGGCTT CCCACAACCC ATCCTTTCCG AAGATGGGAG 1200

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TAGAATCAGA TATGGAGGAC GAGACTACAG CTTGGATGAA TTTGAAGCCA ACAAATCCT1260
 GCACCAGCAC CTCGGGGCCC CTGAAGAGCG GCTTGCTCTT CACATCCTCA GGACTCAGGG1320
 GCTGGTCCCT GAGCAGGTGG AAACAAGGAC TTTGCACAGC ACCTTCCAGC CCAACATTTTC1380
 CCAGGGAAAA CTTCAGATGT GGGTGGATGT TTTCCCCAAG AGTTTGGGGC CACCAGGCCCC1440
 TCCTTTCAAC ATCACACCCC GGAAAGCCAA GAAATACTAC CTGCGTGTGA TCATCTGGAA1500
 CACCAAGGAC GTTATCTTGG ACGAGAAAAG CATCACAGGA GAGGAAATGA GTGACATCTA1560
 CGTCAAAGGC TGGATTCTCT GCAATGAAGA AAACAACAGC AAAACAGATG TCCATTACAG1620
 ATCTTTGGAT GGTGAAGGGA ATTTTAACGT GCGATTGTGT TTCCCGTTTG ACTACCTTCC1680
 AGCCGAACAA CTCTGTATCG TTGCGAAAAA AGACGATTTT TGGAGTATTG ACCAAACGG1740
 ATTTTCAACT CCACCCAGGC TGATCATTCA GATATGGGAC AATGACAAGT TTTCTCTGGA1800
 TGACTACTTG GGTTCCTTAG AACTTGACTT GCGTCACACG ATCATTCTCT CAAAATCACC1860
 AGAGAAATGC AGGTTGGACA TGATTCCGGA CCTCAAAGCC ATGAACCCCC TTAAAGCCAA1920
 GACAGCCTCC CTCTTTGAGC AGAAGTCCAT GAAAGGATGG TGGCCATGCT ACGCAGAGAA1980
 AGATGGCGCC CGCGTAATGG CTGGGAAAGT GGAGATGACA TTGGAATATC TCAACGAGAA2040
 GGAGGCCGAC GAGAGGCCAG CCGGGGAAGG GCGGGACGAA CCCAACATGA ACCCCAAAGCT2100
 GGACTTACCA AATCGACGAG AAACCTCCTT CCTCTGGTTC ACCAACCCAT GCAAGACCAT2160
 GAAGTTCACT GTGTGGCGCC GCTTTAAGTG GGTCTATCAT GCCTTGCTGT TCCTGCTTAT2220
 CCTGCTGCTC TCGTGGCCGC TGCTCCTCTA CTCTTTGCCG AACTATTGTT CAATGAAGAT2280
 TGTAAGCCCA AATGTGTAAC AAAGGCAAGG GCTTCATTTC AAGAGTCATC CAGCAATGAG2340
 AGAATCTCTG CTCTGTAGAC CAACATCCAG TGTGATTTTG TGTCTGAGAC CACACCCAG2400
 TAGCAGGTTA CGCGCTGTCA CCGAGCCCCA TTGATTCCCA GAGGGTCTTA GTCTCGAAA2460
 GTCAGGCCAA CAAGCAAGCT TTGCATCATG TTATCTCTTA AGTATTAATA GTTTTATTT2520
 CTAAAGTTTA AATCATGTTT TTCAAATAT TTTTCAAGGT GGCTGGTTCC ATTTAAAAAT2580
 CATCTTTTTA TATGTGCTTT CGGTTCTAGA CTTCAAGCTT TGGAAATTGC TAAATAGAAT2640
 TCAAAATCTC CTGCACTCTG AGGTGATATA CTTCAATATT GTAATCAACT GAAAGAGCTG2700
 TGCATTATAA AATCAGTTAG AATAGTTAGA ACATTTCTTA TTTATGCCCA CAACCATTTG2760
 TATATTTTGT ATGGATGTCA TAAAGTCTA TTTAACCTCT GTAATGAAAC TAAATAAAAA2820
 TGTTCACCTT TAAACATA GGGGGGGTGG TCGGGGGGTC GGGAGGGGGG GGGGTGCTGT2880
 GGGGTGTGG 2889

(2) INFORMATION ON SEQ ID NO. 400:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1774 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

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TGAAGGAAGT AACAAAGTG GGAACCCCT GATAACCCC CTCAGGATCC TCATGGAGAA 60
CTTACCTATC CAGGAGAAAT AGCAAAGGGG AAAGAAGCTGG CCCCCCCTG ATTCCGATGA 120
CCCTCCCCCC GGGTCCCCCT CCCACAACAT GTGGGAATTC CCAGAGATA AATTCAAGTT 180

GCAATTTTCAG TGGGGACATA GCCCAAACCC ATATCACTGG TGATGCCCAC TTCTTCAGTA 240
TTAGGGGATTC TCAGTCAGAA GAGACCCCTT GTGTGGCCTG AGTCCCCTCA GGAGGAAGGT 300
GGACAACAGA GAAATGAGAG TTTTGATATT TTCTGAAGA GGAACATGTG TTAGAGATGA 360
AGAAATCTCC AAGGCTCATG CAGTTGCTTA GAATAATCAT TACTGTTATA TGAGAAACAT 420
TTTAGTAATT TAATAAARGG ATAATGTTTA TTTAAAAAAC CTGACTTTTC CAGAGTAATT 480
TTGTTTTGCA CATTTCATGT TATTGAAGTG GACTAATTTT TATAATGCAA ATCAGAGTTA 540
AATATTAATA ATTGTGTAATA TACAATTGAC ATAGGAATTA CATTAATAA TTAGGAAGAA 600
ACAAGGACAA ATTTAGACCT TGAATCCGAA GAGATAAAGC TTACTTGACT TTCAAATGGA 660
GAGATGATGA AAACCCACTC ATTCAGTCTT TCAGAACAAA AAGACAGTCA TCTGATAAGA 720
GTATGACATG GATGAAATGC CCTACAGGGG CCTTGGACAT CTTTAATTTT TGCGATTATG 780
TGAAAGAGGT GGACTTTTACA GATAATGGAG CAGAAGCCAA CATTAGTAAA AGGAATCCCA 840
ACTTCTTCCC ATAGAATTAG AATCATGTGA AAGTACAATA AACTTCTTGT TCAAATTACC 900
AGCATCAGAG AGCTTCCCAT TTGCATCTAG ACCTTGAATT TATATTTATT GATCAAGTTC 960
TAATTTGTAT GTATATTTTG TGCATATTCA CCAATAACAG TTAATAATTAA TTATGTGTTA1020
TAGTTAATAT ATGCACCTAC CTCTCTCCGT TAGTGATCA GTAAATGTGT TATTTTGTCA1080
TTTTTCCAAA GAGAGTGTGT TAGGTTTTC CTGTAGTTCT TCCTTTATAG CTTTTCTTCT1140
GATAACCATG ACTTCAGGAG CTTTAAACT ATCTATCTTG CATTTGTGTC TGGCGGAGAA1200
CTAGCCATCA GCCTCCTGAA GCCTGCCATC ATTGTTAATT TGAGGACTGG GCTGTCTTGG1260
GGCTCAGAAG GTAAAGAACT ATTTGAGCAG ATGTGTGTGG GTGGCACTGG ATTCACCCCA1320
ACTGCCAAGT TAGTATTGTT AGAGATTTC TTTTACAACA CAAAAATAAG CCTGTGTCAA1380
AGATTTTAAA ATCATGGAAA GTTAAATCT AGAAGACCT TAGAGAACCA GCCAACCAAC1440
TCTCTCATTT TAAAGTGAA GGATTCATAG CACAGATTAC TTGCCTAAGA TCATCCAGGA1500
ACGAAGACAA GAATCCAAAT GTACTTGGGG ACAAGAATTA GTCCCCAAAT TCAGTGTTC1560
TCCTAGTATT AAACATTGCC CCTTTCGACA AATTTGGAT TTCAACTTTG GTATATTTCA1620
GTAACCTGCT TGATTTATTA GGTACTGGG TAGATGACAT TAGAATGTAG ATAGCGTGCA1680
CGCTATGATA GACTCTGCTA AGACATGTT CCAGTGTCCA GCAGCAATGT AGATATGTGT1740
GACAGTGGTC ATGTAGAAGT TATAAGCAG AGTA 1774

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(2) INFORMATION ON SEQ ID NO. 401:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3982 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

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CCCAAGTGTG ATGCATTGTT CTTCAGATGT TGAAGAAGAAA GCAAAAAATA CTTTCTAACT 60
TAAGACAGAA TTTTAAACAA AATGAGCAGT AAAAGTCACA TGAACCACTC CAAAATCAGT 120
GCATTTTGCA TATTTTAAAA CAAAGACAGC TTGTTGAATA CTGAGAAGAG GAGTGAACAG 180
AGAAGGTCTG TACTAACAAA GCCAAATTCC TCAAGCTCTT ACTGGACTCA GTTCAGAGTG 240
GTGGGCCATT AACCCCAACA TGAATTTTTT CCATATAAAT CTCAATGAAT TCCCTTTTCAT 300

TTGAATAGGC AAACCCAAAT CCATGCAAGT GTTTTAAAGC ACTGTCCTGT CTTAATCTTA 360
CATGCTGAAA GTCTTTCATGG TGATATGCAC TATATTCAGT ATACGTATGT TTTCTCACTT 420
CTCTTGTAAG ACTGTTGCAT GATCCAACCT CAGCAATGAA TTGTGCCTAG TGGAGAACCT 480
CTATAGATCT TAAAAAATGA ATTATTCTTT AGCAGTGTAT TACTCACATG GGTGCAATCT 540
TTAGCCCCAG GGAGGTCAAT AATGTCTTTT AAAGCCAGAA GTCACATTTT ACCAATATGC 600
ATTTATCATA ATTGTGTGCT AGGCTGTATA TTCAAGCCTG TTGCTCTAAC ATTTTGTATA 660
AAAAAGACAA ACAGAAATTA TCTGTCAATT GAGAAGTGGC TTGACRAATCA TTTGAGCTTT 720
GAAGCAGTCA CTGTGGTGTA ATATGAATGC TGTCTAGTGT GTCATAGTAC CAAGGGCAGC 780
TGTCTCCCTT TGTATAACT GATTTCCCTT TTAGTCTCTT ACTGCTAAAT AAGTTAAATTT 840
TGCATTTTGC AGAAAGAAAC ATTGATTGCT AAATCTTTTT GCTGCTGTGT TTTGGTGTTT 900
TCATGTTTAC TTGTTTTATA TTGACTGTTT TAAGTATGAG AGGCTTATAG TGCCCTCCAT 960
TGTAATCCCA TAGTCATCTT TTTAAGCTTA TTGTGTTTAA GAAAGTAGCT ATGTGTTAAA1020
CAGAGGTGAT GGCAGCCCTT CCCTAGCACA CTGGTGGAAAG AGACCCCTTA AGAACCTGAC1080
CCCGATGAAT GAAGCTGATG CACAGGGAGC ACCAAAGGAC CTTCGTAAAG TGATAATTGT1140
CCTGGCCTCT CAGCCATGAC CGTTATGAGG AAATATCCCC CATTCGAATC TAACAGATGC1200
CTCCTCTCCA AAGAGAATTA AAATCGTAGC TTGTACAGAT CAAGAGAATA TACTGGGCAG1260
AATGAAGTAT GTTGTTTTAT TTTTCTTTAA AAATAAAGGA TTTTGGAACT CTGGAGAGTA1320
AGATATAGTA TAGAGTTTGC CTCACACAT GTGAGGGCCA AATAACCTGC TAGCTAGGCA1380
GTAATAAACT CTGTTACAGA AGAGAAAAG GGCCGGGCAC AGTGGCTTAT TCCTGTAATC1440
CCAACACTGT GGAAGGCCGA GGCAGGAGGA TCACCTTGAGT CCAGGAGTTT GAAACCTACC1500
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GTGAGCCATG ATCATGCCAC TGCACTCCAT CCTGGGTGAC AGCAAGATCT TGTAAAAAAA1680
AAAAAAGAAA AAACCCAGAG TGA AAAAGGA AAGTAGAAGG CAGCTGCTGG CCTAGATGTT1740
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TTGACTTTGC CAAAGTGTAG ATAGCCCTTA TCCAGCAGTA TTTTAAGTGG GGAATGCAAC1860
GTGAGGCCAA CTGAACAATT CCCCCTGTGG CTGCCAGAT AGTCACAGT CAAGTTGGAG1920
AGTCTCCTTC CAGCCAGTGA CCTACCCAAA CCTTTTGTTT TGTAAAACCT CTCGTGAAAT1980
ACCCGGAAGC CAGGTTTTCT CACGTGTTT CTAGCTTCTT CAGACTCAGC CCAAAATTAGG2040
AAGTGCAGAA GCACATGATG GTGAAAAACC TAGGATTGGG CAGCCTTCCA GAATGGTATG2100

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GAATCTGAGG GAAGATTAT GTTTCGTTTT GGAGGATAGC TCAAGTTGAA TTTCTTTCC2160
 AGCCAGTTAC CTTTCAACC TACCATACT TTGTACAAC CTACACAAA TACTTAGATA2220
 TTTATTAGAT AGCCCTGAAT TCACTCTAAT TATAACAGG GAGTGTAAAC TGCCCCCAGA2280
 TGTTCCTGGG CTGGGTAAAA GCAGCTGGAG TGAAGCACTC ATTTTCCATA AAGGTAACAA2340
 AGGGCAGCTC AGTGGTTACT CAAGCTCAAA AGGGTTTTTT TAAGAGCAAG CATTTGGTTAA2400
 GTCTGTGTAT ACTGAGTTGG AAGTGATTTC AGCACATTCT TTTTGTAGTG AGTGAAAGTT2460
 CTSAAGCCCC CTTTAAACTT CCTCTGGTGT TTTCAATTATA ATTGGTAGCC ATCTCATGAA2520
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 TCCTCTGGAA GAGACTATCA GCGGCAGGAT TCTCCAGGGA AGACCCATCC CCTAGTGCCA3000
 GAGCTTGCAT CCTGGAGACT AAAGATTGCA CTTTTTTGTA GTTTTTTTGC CAAATGCAAT3060
 CCCATTTCTG TGCCTCTTAG CATGCAGTTA GATTTGGACA AACAAGATTTC CTAAGGAATG3120
 ACTTTATTAA CTATAATATG GTTACAGCTA TTATATAAAT ATATATTCTG GTTATAGTTT3180
 TAATATGGAG ATGTTGTGTG CAATGCTGGC CTGTGGTGGT CTGTGTAATG CTTTAACTTG3240
 TATGGAGGAG GCCAGGCTCA GAGCTGAGAT GTGGCCTGAA CCTTCCCTGT ATCGATCCTT3300
 TAATTTAGAA CTGTCAAGAT GTCACTTTCT CCCCCTCTGC CTTTCTAGTG TATCTGACAT3360
 ATACTCAAAA CAGTAATTTC CTGCTCACAT CATTAACTGC TAATTCGTGA TTTATAAGA3420
 ATTTTCAGAT GGACATGTAC AAATTTGAAC TCAAACCATC CCCAGTCCAG ATACAGGGCA3480
 GCGGTGTAGT GACCACACCA GAGCCTCAGC CTGGTCTCT CTCAGCCGTC GGGATAGGAT3540
 CCAGGCCATTT CTTTAAATC TCAGAGGTAG CAGTAAACTT TTCAGTATTG CTGTTAGCA3600
 GTGTGTGTTT GCCAATAGAT ACCCATTATA CTAATGTGCC AAGTAAATGT TCATTGCACA3660
 TCTGCTTCCA CTGTGTTCCC ACGGTTGCCA TGAAGTGTGT GAGGAGCCCC TCATCTGGAG3720
 GGATGAGTGC TGCCTTGACT ACTGCTATCA GGATTGTGTT GTGTGGAATA TTCATCTACA3780
 TAAATTTTAT ATGCACAGTA ATTCCCTTTT TTATATGTCA AGTAACTATT TGTAAAGTT3840
 ATACTCACAA ATTATTATAA TGATTACTAA TATATTTTTT CCATGTTTCA TTGCCTGAAT3900
 AAAAAGCTTT TACCACGTGT AAAAAAATAA AAAAAAATAA AAAAAATG GAAAAAAG3960
 CTGGGGGGGG GGCCCGGTAG CC 3982

(2) INFORMATION ON SEQ ID NO. 402:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1876 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

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CTCTTGGATC CCCTGGACCA CTGGGCATAC TCGCCATCCT CTCCCGGAGA TCTGGGCAGT 60
TCGCCTGCAT TAGACTTCCT GATTGAGATT CAGTGCATCA GCCGTGCTAT CCATCACGTC 120
CACACCTCTG TGCCCACTCT TGAAGCTGTT GGGAAATATT CAGCAATGTC CGCATCAACT 180
TGCAGAAGAA TATAAATGAC ATTTCAAGGA TAGAAGATAC CTGATTTTTT TTCCTTTTAA 240
TTTTCTGTGT GCCAATTTC AAGTTCCAAGT TGCTAATACA GCAACAATTT ATGAATTGAA 300
TTATCTTGGT TGAAAAATAA AAGATCACTT TCTCAGTTTT CATAAGTATT ATGCTCTCTC 360
TGAGCTATTT CATCTATTTT TGGCAGTCTG AATTTTTTAA ACCCATTTAA ATTTTTTTTC 420
TTACCTTTTT ATTTGCATGT GGATCAACCA TCGCTTTATT GGTGAGATA TGAACATATT 480
GTTGAAAGGT AATTGAGAG AAATATGAAG AACTGAGGAG GAAAAAAAAA AAAAAGAAAA 540
GAACCAACAA CCTCACTGC CTACTCCAAA ATGTTGGTCA TTTTATGTTA AGGGAAGAAAT 600
TCCAGGGTAT GGCCATGGAG TGTACAAGTA TGTGGGCAGA TTTTCAGCAA ACTCTTTTTC 660
CACTGTTTAA GGAGTTAGTG GATTACTGCC ATTCACCTCA TAATCCAGTA GGATCCAGTG 720
ATCCTTACAA GTTAGAAAC ATAATCTTCT GCCTTCTCAT GATCCAACTA ATGCCTTACT 780
CTTCTTGAAA TTTTAACCTA TGATATTTTC TGTGCTGAA TATTTGTTAT GTAGATAACA 840
AGACCTCAGT GCCTTCCTGT TTTTCACATT TTCTTTTCA AATAGGGTCT AACTCAGCAA 900
CTCGCTTTAG GTCAGCAGCC TCCTGAAAGA CCAAAATTAG AATATCCATG ACCTAGTTTT 960
CCATCGTGTG TTCTGACTCT GAGCTACAGA GTCTGGTGAA GCTCACTTCT GGGCTTCATC1020
CGCAACATC TTTATCCGTA GTGGGTATGG TTGACACTAG CCCAATGAAA TGAATTAAAG1080
TGGACCAATA GGGCTGAGCT CTCTGTGGGC TGGCAGTCTC GGAAGCCAGC TTTCCTGCC1140
TCTCATCAAC GAATTAGGTT CAGCATGTCT ATTCAGCTTC GTTTATTTTC AAGAATAATC1200
ACGCTTTTCT GAATCCAAAC TAATCCATCA CCGGGGTGTT TTAGTGGCTC AACATTGTGT1260
TCCCATTTC A GCTGATCAGT GGGCCTCCAA GGGGGGGCTG TAAATGGAG GCCATTGTGT1320
GAGCGTATCA GAGTTGCTGT AAACCTGACC CCGTCTCAGT AAAGCACTG CACCCGCTGT1380
TTATGCTGTG ACACATGGCC CCTCCCTCTG CCAGGAGCTT TGGACCTAAT CCAAGCATCC1440
CTTTGCCGAG AAAGAAGATG GGGGAGGAGG CAGTAATAAA AAGATTGAAG TATTTTGTGT1500
GAATAAAGTC AAATCTTCTT GAACCTCAAC TGAGGAATTT CACCTGTAAA CCTGAGTCGT1560
ACAGAAAGCT GCCTGGGTATA TCCAAAAGCT TTTTATTCTC CTGCTCATTA TTGTGATCTT1620
GCCTTTGGGG ACTTTTCTTA AACCTTCAGT TATGATTTTT TTTTCATACA CTATTGGAA1680
CTCTCTGTGA TTTTGGCCTC TTCCAGTCTT CCTGACACTT TAATTACCAA CTTGTTACCT1740
ACTTTGACTT TTTGCATTTA AAACAGGACA CGGGGCAGGG AGAAAAGGTT TTTAGTTTTT1800
AAACCCGGTG GTTACCATAA CGCGGGGAAA GGTGGCCCAT ACGGGGCGAA CGTTTTGAA1860
AGGTTAAGGG TATTTT

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1876

(2) INFORMATION ON SEQ ID NO. 403:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1216 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

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TCTGTTCTGT  GGGAACACTGT  TACTGTTCTT  CCGTGGCCAA  CCATGGCGGC  CACCAGCCCT  60
ACCCCCGCTC  GGGCCACTTT  CCCTGGACAG  TGCCCTCGCA  GGAGTACTCA  CACCCGCTCC  120
CGCCACACAC  CTCGCTCCCC  CAGTCCCTTC  CCAGCCTGGC  GGTCAGAGAC  TGGCTTGACG  180
CCTCCACAGC  GCCCGGCCAC  CAGGATTTC  ACAGGGTGTA  TGGGCAGCCG  TCCACCAAAC  240
ACTACGTGAC  GAGCTAACGC  CACGCAGGCG  GCGGGGCGCT  GGGGAATCTT  CCTCCCCAGC  300
CCCCGGGCTC  GGGAGTTATG  CATCCAGAGA  CCTGCCCTTC  TACCTTCTCT  GCCTCCCCCT  360
TTECTCATTC  CATGCCCCCA  GGTCTTTTCC  TTTTGGATTT  TGTTTTGGTT  TTGGCTTTGT  420
TTTTGATTTT  TTTTATTAT  GAATCTCCTG  GACGCAGAGG  TGACAGTGGG  AGCTGGCCTG  480
GGCCAGGACG  GCAGGTGGCC  CTGGAGATGG  GAAAGTGTCT  GTGTGAGGCC  GCTGAGCTCT  540
CTCTCTGTTT  CTCCTTTTTT  CCTCTACTCC  TTCCCCCTCA  CACCCCCGTG  GCTGGAAGGA  600
ACCTCGGCTT  CCGTGAAAGC  TTGGGGGTCC  CACCCCTCTT  ACCCCACCCG  GGAGGAACGC  660
CCAGGGCCCC  GGGCTTGTCT  CTCCTCTTGT  TTTCTTTTGG  GGCAGTTTGA  TCACTGATCG  720
AGTAAGGAAT  GACCTTTAGA  TTGTGCGACT  TTTGTTTTTG  TTTTTTAAAT  TTTTTTAAAT  780
CCAAGAATGA  TTTCTCCTGC  TTCTCTCTCC  TCACCATCTT  CCCAGACGGA  GTTCAAAGGC  840
CACTTCTCAA  GCAGCTTTTG  GCACCTTCAG  CCTCAGAGTG  GAATCTTTTA  AAGACAGGAC  900
CCCTATGTCC  AGGAAAGGGG  AAAAGGAAC  TTGCCAATGA  TAGTGACCAC  AGCAAAAGCA  960
ATAAAATAT  AAAATAAAAA  ACRAATAGCAC  AGCCCTTGTT  GAGGTCAGCA  GGGAGGAGGG  1020
GCTGCCCGGA  GTTGGGTCTT  TGCCCTGGAT  TTGACACAGC  AACTTCTCTG  AGTGAGCACT  1080
TTGTATGAAT  CGTGGACTTC  CTGTTCTCAA  GCGCAGGTA  TTTATTCTGT  ATCTGTCTAG  1140
AGCACACACC  AAAATCCAAC  CTCTAATAA  ACATGATGGC  GCAGTCCCAA  AAAAAAGAAA  1200
CAGAAGAAAG  AAAGGG

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1216

(2) INFORMATION ON SEQ ID NO. 404:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 271 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

RPRAGASIST LAGLSLKEGE DQKEIKIEPA QAVDEVEPLP EDYYTRPVNL TEVTTLQQR 60
 LQPDFQPVCA SQLYPRHKKL LIKRSRLCRK CEHNLSKPEF NPTSIKFKIQ LVAVNYIPEV120
 RIMSIPNLRY MKESQVLLTL TNPVENLTHV TLFECEEGDP DOINSTAKVV VPKELVLAG180
 KDAAAEYDEL AEPQDFQDDP DIIAFRKANK VGIFIKVTPQ REEGEVTVCF KMKHDFKNLA240
 APIRPIEESD QGTEVIWLTQ HVLSLGLPLL P 271

(2) INFORMATION ON SEQ ID NO. 405:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 133 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

DLKQDQGGKQK ICIFLKSGLH LITILLQKTR CSWWSTLSSF ILENIIIEIKV SNPTPGYQVK 60
 TASLLLGQNC GLLAELFYGL QSKWSYLTHH MTKVLNLVRG KVLNIQFWIQ EIIIVNFPFK120
 SMERMLVENI LKI 133

(2) INFORMATION ON SEQ ID NO. 406:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

RGPGHLLKPN GGPPMKLGYG RNLDISPRLE LNRETVKRSI RFHRFWPLIP NSFPHNSVFL60
 VSMKCLESHR KPVKIFLKKK KPQKTDHLSI QWTSI 95

(2) INFORMATION ON SEQ ID NO. 407:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

YLSLCPCWPG NFFQWCLLEE VFSSCHFKEI KLEIEYGWHD CTLLVLLFFY SSVPL 55

(2) INFORMATION ON SEQ ID NO. 408:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

LQEAPCGEHG RHLHKSAMRR DTESELHHQR QVQGAETVGS GQGSAAFSGP SPYARGPGPD 60
LPLLGGQHLS IRRWFKCVTM SQCVLELPFS NANLPSLHIS PHPWTRFCVS ESGNLLKRGGL20
STPGLLV 127

(2) INFORMATION ON SEQ ID NO. 409:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 95 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

KGVGLLIMGG QGQVLGHRER VRRMLQTPAH CPRSPLPAPA SDGAALIPCL SSLQIYGAY60
HVLHKELPEV TNSVFHEINM WVSQRTATAG TASPF 95

(2) INFORMATION ON SEQ ID NO. 410:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 296 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

VVLAPTFGH YVCTVISHAH EVRQMQLERR VRSGVMSEKD HMVIMHDVLD AQWLYDNHKD 60
ESYLRRVVP LEKLLTSHKR LVMKDSAVNA ICYGAKIMLP GVLAYEDGIE VNQEIVVITT120
KGEAICMAIA LMTTAVISTC DHGIVAKIKR VIMERDTYPR KWGLGPKASQ KKLMIKQGLL180
DKHGKPTDST PATWKQEVD YSESAKKEVV AEVVKAPQVV AEAAKTAKGS EESESESDT240
PPAAPQLIKK EKKKSKKDKK AKAGLESAGAE PGDGDSDTTK KKKKKKKAKE VELVSE 296

(2) INFORMATION ON SEQ ID NO. 411:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 280 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

RQGGGSLRS FPLRWTRHD AVQGNMADAE VIILPKKHKK KKERKSLPEE DVAEIQHAE 60
 FFIKPEKVA KLDTSQWELL LKNFDKLNVR THTYPLACG SNPLKREIGD YIRTGFIND120
 KPSNFSHEV VAWIRAILRV EKTGHSGTLD PKVTGCLIVC IERATRLVKS QQSAGKEYVGI80
 IVRLHNAIEG GTQLSRALET LTGALFQRFP LIAAVKRQLR VRTIYESKMI EYDPERRLGI240
 FVVSCEAGTY IRTLCHVSDQ SRARGTSDAG ASEGFSWSHE 280

(2) INFORMATION ON SEQ ID NO. 412:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 360 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

RHPHPEGVMG FSRGCGSASS ILWKPDHCFW QRFPGHQEFE EERLRPAGMH GTQRGRGGQV 60
 DPAAHCPGAH GETHLPDPQ REDRGHGGAT TFSLNCSAAG TPTPSLVWVL PNGTDLQSGQ120
 QLQRFYHKAD GMLHISGLSS VDAGAYRCVA RNAAGHTERL VSLKVGLKPE ANKQYHNLS180
 IINGETLKLFP CTPPGAGQGR FSWLTPNGMH LEGPQTLGRV SLDDNGTLTV REASVFDRT240
 YVCRMETEGY PSVTSIPVIV IAYPPRITSE PTFVIYTRPG NTVKLNCMAM GIPKADITWE300
 LPDKSHLKAG VQARLYGNRF LHPQGSLLTQ HATQRDAGFY KCMARNILGS DSKTTYIRVF360

(2) INFORMATION ON SEQ ID NO. 413:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 314 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

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EEGDYTCFAE  NQVGKDEMRY  RVKVVVTAPAT  IRNKTYLAVQ  VPYGDVVVTA  CEAKGEPMKP  60
VTWLSPTNKV  IPTSSEKYQI  YQDGTLLIQK  AQRSDSGNYT  CLVRNSAGED  RKTVVIHVNV  120
QPPKINGNPN  PITTVREIPA  GGSRKLECK  AEGIPTPRVL  WAFPEGVVLP  APYYGNRITV  180
HGNGSLDIRS  LRKSDSVQLV  CMARNEGGEA  RLILQLTVLE  PMEKPIFHDP  ISEKITAMAG  240
PQHSASTALP  RGP RHPAWCG  SFPMAPICRV  DSSCSASTTR  LTACYTLAVS  PRWTLGP TAA  300
WPAMPLATRR  GWSP

```

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(2) INFORMATION ON SEQ ID NO. 414:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

```

RPVPAKLNPR  SWPRTAGALP  LRPPPLTMAV  FHDEVEIEDF  QYDEDESETYF  YPCPCGDNFS  60
ITKEDLENGE  DVATCPSCSL  IIKVIYDKDQ  FVCGETVPAP  SANKELVKC

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109

(2) INFORMATION ON SEQ ID NO. 415:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

YAKSTATSHG NLTLTPTWNA ISLALSKHKQ KLRYNITCS DLAKSFKHST YYTGMLCSSH 60
SVTNFTSFGC FSPHLVLTSK EYAEYKKSPP SFITSFWTF L VH 103

(2) INFORMATION ON SEQ ID NO. 416:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 144 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

YTMKIIYFTR KILYXQGGIL KYNTGXSFL LYIMIVSFHI SWXLXGKGT XKSIFIYIKT 60
KCKXQRLXPP KCLVSLNNM NEXKMNQIT WXTHRRXNKX AQEIKSCFKL GHIKGGKGS120
RRVRKISSQA TKNLXRRQPP NXIR 144

(2) INFORMATION ON SEQ ID NO. 417:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 74 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

LILMGRLIYN XNYLFYKXDS IHXGRHLEVQ YTRXFISLSLH YDCEFPYKLX TXHXXGNXKI60
 HFYIHKNKTX PXET 74

(2) INFORMATION ON SEQ ID NO. 418:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 121 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

YFFFTLCQRN RVFDISSYVK EMLQNVNCFK LKLPKRPRY IYLVYIMFN ICQSILQVCS 60
 FISIKYGYV AQLLKWYCIY YICTPNNIVC TFCFLYCICA GFFRLYQCNL CLLRYVQKMS120
 I 121

(2) INFORMATION ON SEQ ID NO. 419:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 114 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

FFFFFFFFS FQRIHFFFFFF FFFFEKGKVI YLHCFHSSTV VLGLNISITL LFPIYILLEY 60
 YYKYNIQFKK TYGETQLMEF SPLYRLLSII RLQWKFIWTF SVHILKGRDY TDKA 114

(2) INFORMATION ON SEQ ID NO. 420:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 765 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

```
IRPVVQLTAI EILAWGLRNM KNFQMASITS PSLVVECGGE RVESVVIKNL KKTPNFPSSV 60
LFMKVFLPKE ELYMPPLVIK VIDHRQFGRK PVVGQCTIER LDRFRCDPYA GKEDIVPQLK120
ASLLSAPPCR DIVIEMEDTK PLLASKLTEK EEEVDWWSK FDASSGEHEK CGQYIQKGYS180
KLKIYNCELE NVAEFGELTD FSDTFKLYRG KSDENEDPSV VGEFKGSFRI YPLPDDPSVP240
APPRQFRELP DSVPQECTVR IYIVRGLELQ PQDNNGLCDP YIKITLGKKV IEDRHHYIPN300
TLNBPVFGMY ELSCYLPQEK DLKISVYDYD TFRDEKVGE TIIDLENRFL SREGSHCGIP360
EEYCVSGVNT WRDQLRPTQL LQNVARFKGF PQPILSEDSG RIRYGGRDYS LDEFEANKIL420
HQHLGAPPEER LALHILRTQG LPVEHVETRT LHSTFQPNIS QGKLQMWVDV FPKSLGPPGP480
PFNITPRKAK KYLLRVIIWN TKDVILOEKS ITGEEMSDIY VKGWIPGNEE NKQKTDVHYR540
SLDGGGNNFN RVVFPPDYLP AEQLCIVAKK EHFWSIDQTE FRIPPRLIQ IWNDKDFSLD600
DYLGFLELDL RHTIIPAKSP EKCRLDMIPD LKAMNPLKAK TASLFEQKSM KGWWPCYAEK660
DGARVMAGKV EMTLEILNEK EADERPAGKG RDEPNMNPCL DLPNRPETSF LWFTNPFCKTM720
KFIVWRFRKW VIIGLLLELI LLEFVAVLLY SLPNYSMKI VKPNV 765
```

(2) INFORMATION ON SEQ ID NO. 421:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 289 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

```
ETQVVIQRKL VIVPYLNDQP GWDSKFRLVN TPEMLFFRND TELFGWKVVK RENKSPVKIP 60
FTIQRSVMDI CFLFVFFIAR NPAFDVDVTH FLSCDAFLVQ DNVLGVFPDH TQVVLGFFG120
CDVERRAWWP QTLGSEIHHP LKFSGLNVGL EGAVQSPCFH VLRDQLSPFE DVKSKPLFRG180
PEVLVQDFVG FFFIQAVVSS SISDSTPIFG KDGLWEAFES GDILKQLCWS QLISPGIDSR240
NTVLLWYAAV GPKAGKESVF QINNCTSYFF IPGKGVIID RNQVQFFLR 289
```

(2) INFORMATION ON SEQ ID NO. 422:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

FFLYSFSSDN HDFSFKTIY LAFVSGGELA ISLLKPAIIV NLRITGLSWGSG EGKELFEQMC60
VGGTGFHPTA KLVLEISFY NTKISLCQRF 90

(2) INFORMATION ON SEQ ID NO. 423:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

TPSGSSSWRTY LSRNSKGER TGPPLIPMTL PPGPLPTTCG NSQKINSSCN FSGDIAQTHI60
TGDAHFFSIR DSQSEETPCV A 81

(2) INFORMATION ON SEQ ID NO. 424:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

ENWASRYFQS SFTEQKVWVG HWLEGDSPTL TVTIWAATGG IVQLASRCIP HLKVCWIKAI 60
YTLAKSKAKE IALDPESQQD HLIFPNQHLG QQLPSTFLFH SWFFFFFELQ DLAVTQDGVQ120
WHDHGSLLQP 129

(2) INFORMATION ON SEQ ID NO. 425:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 122 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

EAQKWDCIWT KNYKKVQSLV SRMQALALGD GSSLENPAAD SLFQRRSFER RVCYISFFTV 60
TLWRLKDLVV SCFLKITGIW RPKPFWTDI SSKYFFIKVF EGDDFLDLWL DILGFDPYIV120
LS 122

(2) INFORMATION ON SEQ ID NO. 426:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 105 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

REFKSPQRQN HNMSRRNKKL LDIPGSFLYD SGLQVKFSL SSEEFELIPA KYFNLFITAS 60
SPIFFLGKGM LGLGPKLLAG GGAMCHSITD GCKCFTEQGS GLQQ 105

(2) INFORMATION ON SEQ ID NO. 427:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

EKYEELRRKK KKKKRTNNLN CLLQNVG:FM LREEFQGMAM ECTSMWADFQ QTLFPLFKEL60
VDYCHSLHNP VGSSDPYKLE NIIFCLLMIQ LMPYSS 96

(2) INFORMATION ON SEQ ID NO. 428:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

RKKGETEREL SASTQTLSHL QGHLPSWPRP APTVTSASRR FIIKKNQKQS QNQNKIQKEK 60
TWNGMRKRG GEEGRAGLW MHNSRARGLG RKIPQRPAAC VALARHVVEG GRLEIHPVEI120
LVAGLLGGVK PVSQRQAGKG LGDGGCGRER V 151

(2) INFORMATION ON SEQ ID NO. 429:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

```
RHAGGGALGN LPPQPPGSGV MHPETCPSTF LASPLPHSIA PGLFLDFFVL VLALFLIFFY 60
YESPGRRGDS GSWPGPGRQV ALEMKGKLCR GAELSLCFSF FPLLLPLHTP VAGRNLGFPPE120
SLGVPPFLPH PGGTPRAPGL FLLLSFWAV                                     150
```

(2) INFORMATION ON SEQ ID NO. 430:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 285 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

```
SWRTGGWAYA GDRLENKTSV SVASWASSLN ARMDNRFATA FVIACVLSLI STIYMAASIG 60
TDFWYEYRSP VQENSSDLNK SIWDEFISDE ADEKTYNDAL FRYNGTVGLW RRCITIPKMN120
HWYSPPERTE SFDVVTCKVS FTLTEQFMEX FVDPGNHNSG IDLLRITYLWR CQFLLPFVSL180
GLMCFGALIG LCACICRSly PTIATGILHL LAGLCTLGSV SCYVAGIELL HQKLELPDNV240
SGEFGWSFCL ACVSAPLQFM ASALFIWAAH TNRKEYTLMK AYRVA                      285
```

(2) INFORMATION ON SEQ ID NO. 431:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 116 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

LCPEFWAIPM HVFGYGDTPS PQSHCAIVSK KCIILSLFIC LITNEFIPDA FIQITGIFLN 60
WTSIFIPEVC ANGGCHVDGG NEAKHTSNYK CCSKTVIHSG IQTARPGCYG DRGLVL 116

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Claims

1. A nucleic acid sequence that codes a gene product or a portion thereof, comprising

- a) a nucleic acid sequence, selected from the group Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, 391-403,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-127 and 391-403, or a complementary or allelic variant thereof.

3. Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403, characterized in that they are expressed elevated in normal bladder tissue.

4. BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 for use as vehicles for gene transfer.

5. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

6. A nucleic acid sequence according to claims 1 to 4, wherein it has % homology to a human nucleic acid sequence.

7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a

sufficient amount that they hybridize with the sequences according to claims 1 to 6.

8. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. A nucleic acid sequence according to one of claims 1 to 9, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 9, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to one of claims 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

15. A DNA fragment, comprising a gene, that can be obtained from the use according to claim 14.

16. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to one of claims 1 to 10.

17. Host cell according to claim 16, wherein it is a prokaryotic or eukaryotic cell system.

18. Host cell according to one of claims 16 or 17, wherein the prokaryotic cell system is *E. coli*, and the eukaryotic cell system is an animal, human or yeast cell system.

19. A process for producing a polypeptide or a fragment, wherein the host cells according to claims 16 to 18 are cultivated.

20. An antibody that is directed against a polypeptide or a fragment that is coded by the nucleic acids of sequences Seq. ID Nos. 1-127 and 391-403, which can be obtained according to claim 19.

21. An antibody according to claim , wherein it is monoclonal.

22. An antibody according to claim , wherein it is a phage display antibody.

23. Polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431.

24. Polypeptide partial sequences according to claim 23, with at least 80% homology to these sequences.

25. A polypeptide that is known from a phage display and that can bind to the polypeptide partial sequences according to claim 23.

26. Polypeptide partial sequences according to claim 23, with at least 90% homology to these sequences.

27. Use of polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431 as tools for finding active ingredients against the bladder tumor.

28. Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 for expression of polypeptides that can be used as tools for finding active ingredients against the bladder tumor.

29. Use of nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 in sense or antisense form.

30. Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 as pharmaceutical agents in gene therapy for treatment of the bladder tumor.

31. Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 for the production of a pharmaceutical agent for treatment of the bladder tumor.

32. Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431.

33. A nucleic acid sequence according to claims 1 to 10, wherein it is a genomic sequence.

34. A nucleic acid sequence according to claims 1 to 10, wherein it is an mRNA sequence.

35. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403.

36. Use of the genomic genes according to claim 33, together with suitable regulatory elements.

37. Use according to claim 36, wherein the regulatory element is a suitable promoter and/or enhancer.

38. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 300 to 3500 bp.

Abstract

Human nucleic acid sequences -- mRNA, cDNA, genomic sequences -- from normal bladder tissue, which code for gene products or portions thereof, and their use, are described.

In addition, the polypeptides that can be obtained by way of the sequences and their use are described.

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Systematic Gene Search in the Incyte LifeSeq Database

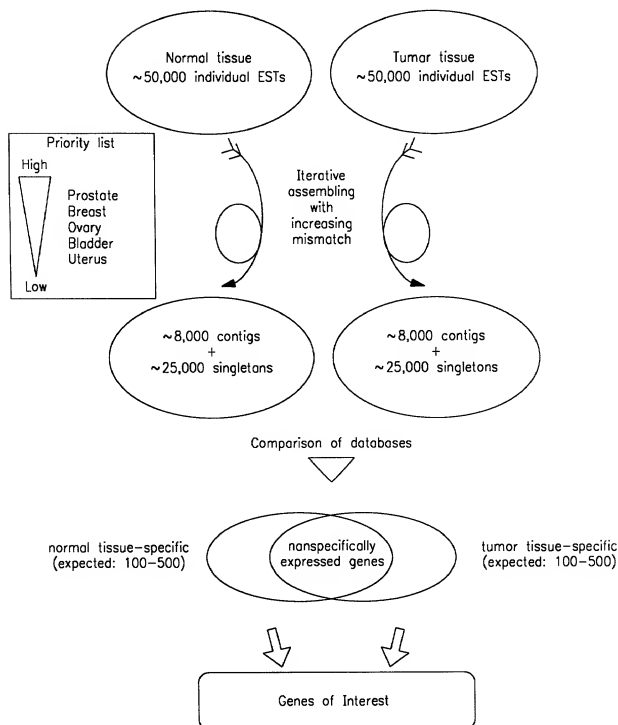
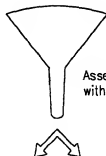


FIG. 1

Principle of EST Assembly

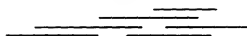
~50,000 ESTs per tissue



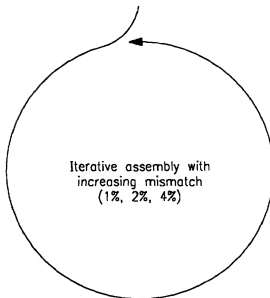
Assembly at 0% mismatch
with GAP4 (Staden)

Contigs

Singletons



Contigs increasing in
number and length



Iterative assembly with
increasing mismatch
(1%, 2%, 4%)

5000-6000 Contigs

~25,000 other singletons



~30,000 consensus-
sequences per tissue

FIG. 2a

~50,000 ESTs
of a tissue
(e.g.: uterus tumor)

GAP4 Assembly 1st Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 0

GAP4-Database 1:
Contigs 1 Singletons 1

unassembled
ESTs

GAP4 Assembly 2nd Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 1

GAP4-Database 2:
Contigs 2 Singletons 2

unassembled
ESTs

GAP4 Assembly 3rd Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 2

GAP4-Database 3:
Contigs 3 Singletons 3

unassembled
ESTs

FIG. 2b-I

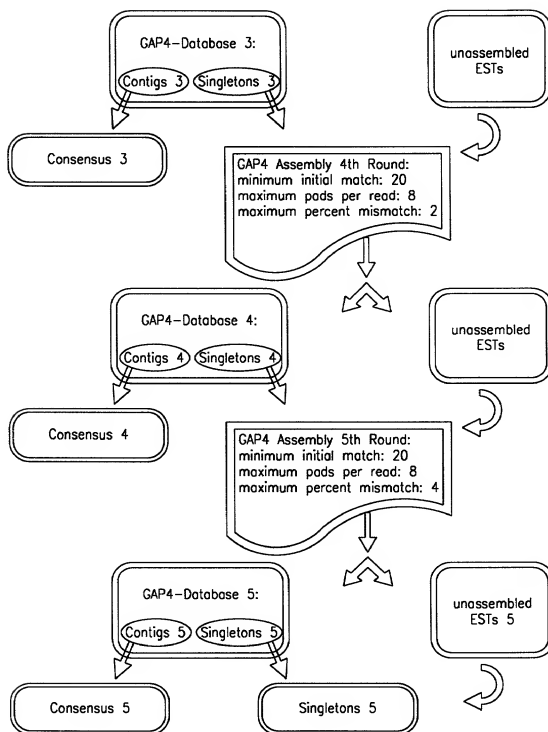


FIG. 2b-2

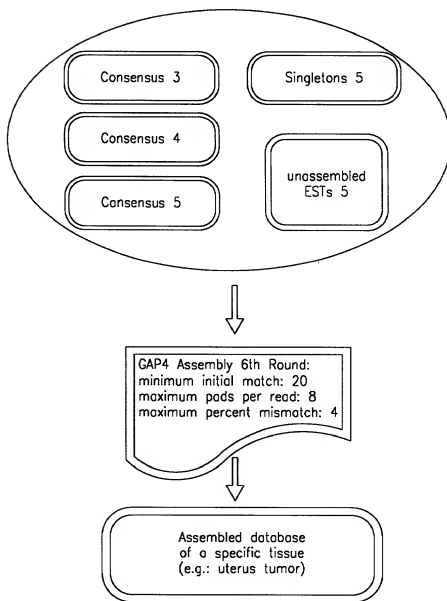


FIG. 2b-3

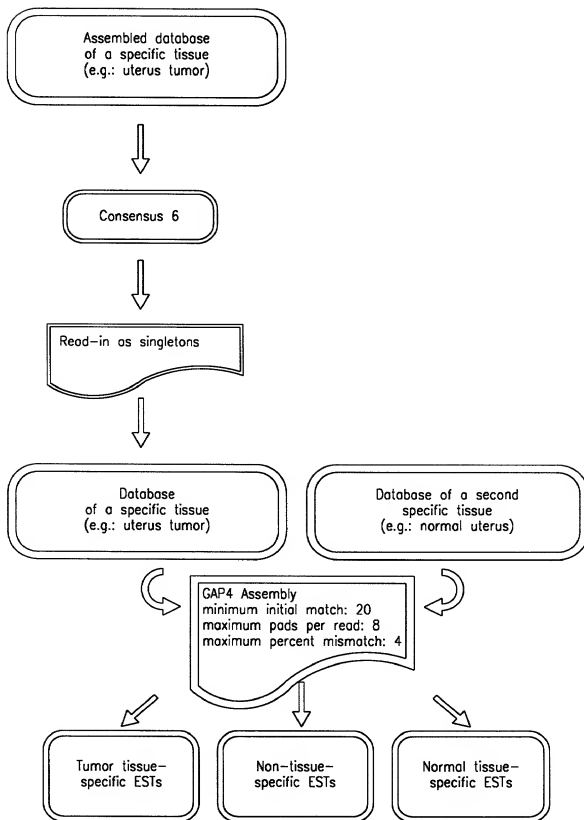
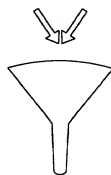


FIG. 2b-4

In silico subtraction of gene expression in various tissues

~30,000 consensus sequences
normal tissue

~30,000 consensus sequences
cancer tissue



Assembly at 4% mismatch

Normal tissue
Specific genes

Cancer tissue
Specific genes

Genes expressed in both tissues

FIG. 3

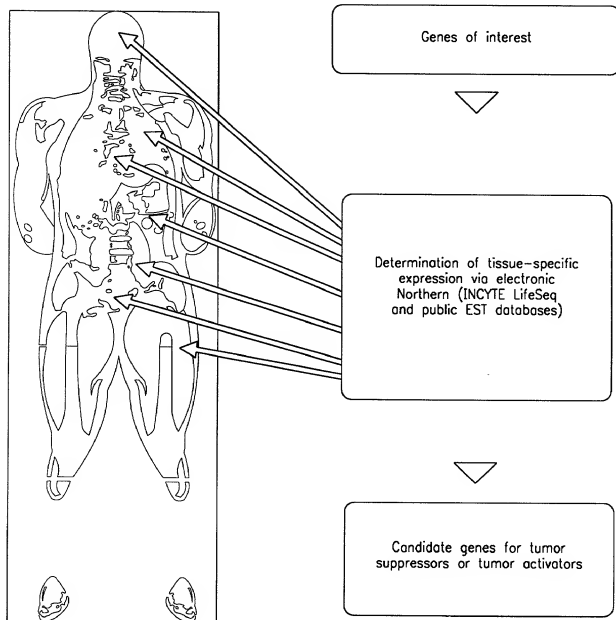


FIG. 4a

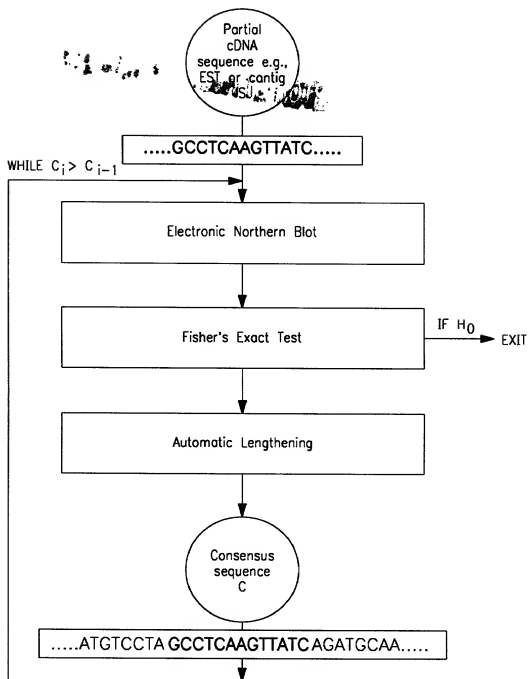


FIG. 4b

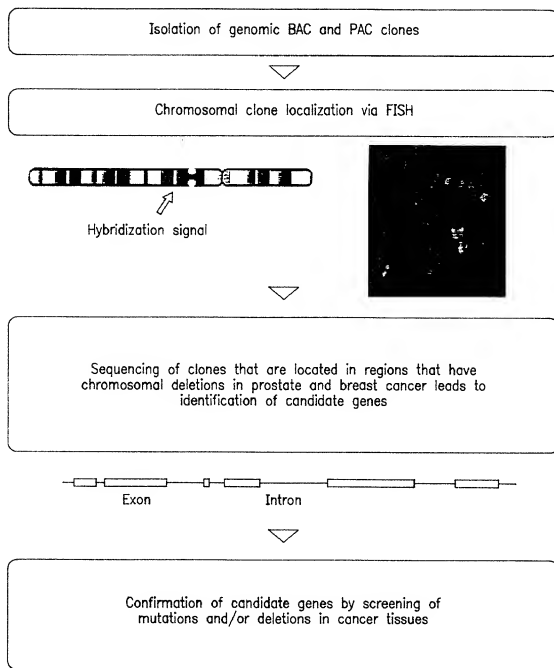


FIG. 5

Attorney Docket Number: SCH 1781**DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

HUMAN NUCLEIC ACID SEQUENCES OF NORMAL BLADDER TISSUE

the specification of which

☐ is attached hereto

☒ was filed on 15 April 1999 as United States Application Number or PCT International Application Number PCT/DE99/01163 and (if applicable) was amended on _____

I hereby authorize our attorneys to insert the serial number assigned to this application.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56.

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT international application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT international application having a filing date before that of this application on which priority is claimed.

| PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119 | | | |
|----------------------------------------------------------------------------|---------|----------------------|------------------|
| APPLICATION NO. | COUNTRY | DAY/MONTH/YEAR FILED | PRIORITY CLAIMED |
| 198 18 620.7 | Germany | 21 April 1998 | X |
| | | | |

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

| PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e) | |
|----------------------------------------------------|-------------|
| APPLICATION NUMBER | FILING DATE |
| | |

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT international application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT international application in the manner provided by the first paragraph of 35 U.S.C. §112.

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| PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120 | | |
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I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I. William Millen (19,544); John L. White (17,746); Anthony J. Zeiano (27,969); Alan E.J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brion P. Heaney (32,542); Richard J. Taverro (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460); Nancy J. Axelrod (44,014); James E. Ruland (40,921) and Jennifer J. Branigan (37,432).

Declaration for Patent Application (Continued)

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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51587AWO MAXX24-P

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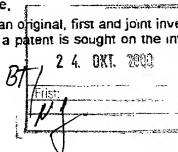
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